



## SEQUENCE LISTING

<110> COOKE, DAVID  
DEBET, MARTINE  
GIDLEY, MICHAEL, JOHN  
JOBBLING, STEPHEN, ALAN  
SAFFORD, RICHARD  
SIDEBOTTOM, CHRISTOPHER, MICHAEL  
WESTCOTT, ROGER, JOHN

<120> IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION

<130> 054163-5003-US

<140> 10/056,454  
<141> 2002-01-24

<150> PCT/GB96/01075  
<151> 1996-05-03

<150> GB 9607409.1  
<151> 1996-04-10

<150> GB 9509229.2  
<151> 1995-05-05

<160> 43

<170> PatentIn version 3.2

<210> 1  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 1  
aaggatccgt cgacatcgat aatacgactc actataggga tttttttttt ttttttt 57

<210> 2  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 2  
aaggatccgt cgacatc 17

<210> 3  
<211> 17  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide  
  
<400> 3  
gacatcgata atacgac 17  
  
<210> 4  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide  
  
<400> 4  
catccaacca ccatctcgca 20  
  
<210> 5  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide  
  
<400> 5  
ttgagagaag atacctaagt 20  
  
<210> 6  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide  
  
<400> 6  
atgttcagtc catctaaagt 20

<210> 7  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 7  
 agaacaacaa ttcctagctc 20

<210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 8  
 ggggccttga actcagcaat 20

<210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 9  
 cgtcccagca ttcgacataa 20

<210> 10  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 10  
 cttggatcct tgaactcagc aatttg 26

<210> 11  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 11  
 taactcgagc aacgcgatca caagttcgt

29

<210> 12  
 <211> 3003  
 <212> DNA  
 <213> Solanum tuberosum

<400> 12  
 gatggggcct tgaactcagc aatttgacac tcagttagtt acactgccat cacttatcag 60  
 atctctatTTt tttctcttaa ttccaaccaa ggaatgaata aaaagataga tttgtaaaaa 120  
 ccctaaggag agaagaagaa agatgggtgta tacactctct ggagttcgtt ttcctactgt 180  
 tccatcagtg taaaaatcta atggattcag cagtaatggg gatcggagga atgctaatat 240  
 ttctgtattc ttgaaaaaac actctctttc acggaagatc ttggctgaaa agtcttctta 300  
 caattccgaa tcccgacctt ctacaattgc agcatcgggg aaagtccttg tgcttggaat 360  
 ccagagtgat agctcctcat cctcaacaga tcaatttgag ttcgctgaga catctccaga 420  
 aaattcccca gcatcaactg atgtagatag ttcaacaatg gaacacgcta gccagattaa 480  
 aactgagaac gatgacgttg agccgtcaag tgatcttaca ggaagtgttg aagagctgga 540  
 ttttgcttca tcaactacaac tacaagaagg tggtaaactg gaggagtcta aaacattaaa 600  
 tacttctgaa gagacaatta ttgatgaatc tgataggatc agagagaggg gcatccctcc 660  
 acctggactt ggtcagaaga tttatgaaat agacccctt ttgacaaact atcgtcaaca 720  
 ccttgattac aggtattcac agtacaagaa actgaggagg gcaattgaca agtatgaggg 780  
 tgggttgga gctttttctc gtgggtatga aagaatgggt ttcactcgtg gtgctacagg 840  
 tatcacttac cgtgagtggg ctectgggtgc ccagtcagct gccctcattg gggatttcaa 900  
 caattggggac gcaaatgctg actttatgac tcggaatgaa tttgggtgtc gagagatttt 960  
 tctgccaaat aatgtggatg gttctcctgc aattcctcat ggggccagag tgaagatacg 1020  
 tatggacact ccatcaggtg ttaaggattc cattcctgct tggatcaact actctttaca 1080  
 gcttctgat gaaattccat ataattggaat atattatgat ccacccgaag aggagaggta 1140  
 tatcttccaa caccacggc caaagaaacc aaagtcggtg agaatatatg aatctcatat 1200  
 tggaatgagt agtccggagc ctaaaattaa ctcatacgtg aatttttagag atgaagtctc 1260  
 tcctcgcata aaaaaagctt gggtagaatg cgggtgcaaat tatggctatt caagagcatt 1320  
 cttattatgc tagttttggg tatcatgtca caaatttttt tgcaccaagc agccgttttg 1380  
 gaacgcccga cgaccttaag tctttgattg ataaagctca tgagctagga attgtgtgtc 1440  
 tcatggacat tggtcacagc catgcatcaa ataatacttt agatggactg aacatgtttg 1500  
 acggcacaga tagttgttac tttcactctg gagctcgtgg ttatcattgg atgtgggatt 1560  
 tccgcctctt taactatgga aactgggagg tacttaggta tcttctctca aatgcgagat 1620  
 ggtggttgga tgagttcaaa tttgatggat ttagattcga tgggtgtgaca tcaatgatgt 1680  
 gtactcacca cggattatcg gtgggattca ctgggaacta cgaggaatac tttggactcg 1740  
 caactgatgt ggatgctgtt gtgtatctga tgctgggtcaa cgatcttatt catgggcttt 1800  
 tcccagatgc aattaccatt ggtgaagatg ttagecgaat gccgacattt tgtgttcccg 1860  
 ttcaagatgg ggggtgttggc tttgactatc ggctgcatat ggcaattgct gataaatgga 1920  
 ttgagttgct caagaaacgg gatgaggatt ggagagtggg tgatattgtt catacactga 1980  
 caaatagaag atggtcggaa aagtgtgttt catacgtcga aagtcatgat caagctctag 2040  
 tcggtgataa aactatagca ttctggctga tggacaagga tatgtatgat tttatggctc 2100

tggatagacc	gtcaacatca	ttaatagatc	gtgggatagc	attacacaag	atgattaggc	2160
ttgtaactat	gggattagga	ggagaaggg	acctaaat	catgggaaat	gaattcggcc	2220
accctgagtg	gattgatttc	cctagggctg	aacaacacct	ctctgatggc	tcagtaattc	2280
ccagaaacca	attcagttat	gataaatgca	gacggagatt	tgacctggga	gatgcagaat	2340
atttaagata	ccgtgggttg	caagaatttg	accgggctat	gcagtatctt	gaagataaat	2400
atgagtttat	gacttcagaa	caccagttca	tatcacgaaa	ggatgaagga	gataggatga	2460
ttgtatttga	aaaaggaaac	ctagtttttg	tctttaat	tcaactggaca	aaaggctatt	2520
cagactatcg	cataggctgc	ctgaagcctg	gaaaatacaa	ggttgccttg	gactcagatg	2580
atccactttt	tgggtggcttc	gggagaattg	atcataatgc	cgaatatttc	acctttgaag	2640
gatggtatga	tgatcgtcct	cggtcaatta	tgggtgatgc	acctagtaga	acagcagtgg	2700
tctatgcact	agtagacaaa	gaagaagaag	aagaagaaga	agtagcagta	gtagaagaag	2760
tagtagtaga	agaagaatga	acgaacttgt	gatcgcgttg	aaagatttga	acgccacata	2820
gagcttcttg	acgtatctgg	caatattgca	ttagtcttgg	cgggaatttca	tgtgacaaca	2880
ggtttgcaat	tctttccact	attagtagtg	caacgatata	cgcagagatg	aagtgtgtaa	2940
caaaaacata	tgtaaaatcg	atgaatttat	gtcgaatgct	gggacgatcg	aattcctgca	3000
gcc						3003

&lt;210&gt; 13

&lt;211&gt; 2975

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 13

ttgatgggccc	ttgaactcag	caatttgaca	ctcagttagt	tacactccta	tcacttatca	60
gatctctatt	ttttctctta	attccaacca	ggggaatgaa	taaaaggata	gatttgtaaa	120
aaccctaagg	agagaagaag	aaagatgggtg	tatatactct	ctggagttcg	ttttcctact	180
gttccatcag	tgtacaaatc	taatggattc	agcagtaatg	gtgatcggag	gaatgctaata	240
gtttctgtat	tcttgaaaaa	gcactctctt	tcacggaaga	tcttggctga	aaagtcttct	300
tacaattccg	aattccgacc	ttctacagtt	gcagcatcgg	ggaaagtcct	tgtgcctgga	360
accagagtg	atagctcctc	atcctcaaca	gaccaatttg	agttcactga	gacatctcca	420
gaaaattccc	cagcatcaac	tgatgtagat	agttcaacaa	tggaacacgc	tagccagatt	480
aaaactgaga	acgatgacgt	tgagccgtca	agtgatctta	caggaaagtg	tgaagagctg	540
gattttgctt	catcactaca	actacaagaa	gggtggtaaac	tggaggagtc	taaaacatta	600
aatacttctg	aagagacaat	tattgatgaa	tctgatagga	tcagagagag	gggcatccct	660
ccacctggac	ttggtcagaa	gatttatgaa	atagaccccc	ttttgacaaa	ctatcgtcaa	720
caccttgatt	acaggtattc	acagtacaag	aaactgaggg	aggcaattga	caagtatgag	780
gggtggtttg	aagcttttct	cggtggttat	aaaaaatggg	tttcaactcg	agtgtacag	840
gtatcactta	ccgtgagtg	gctcctgggtg	cccagtcagc	tgccctcatt	ggagatttca	900
acaattggga	cgcaaatgct	gacattatga	ctcggaatga	atttggtgtc	tgggagattt	960
ttctgccaaa	taatgtggat	ggttctcctg	caattcctca	tgggtccaga	gtgaagatac	1020
gtatggacac	tccatcaggt	gttaaggatt	ccattcctgc	ttggatcaac	tactctttac	1080
agcttcctga	tgaatttcca	tataatggaa	tatattatga	tccacccgaa	gaggagaggt	1140
atatcttcca	acacccacgg	caaagaaaac	caaagtcgct	gagaatatat	gaatctcata	1200
ttggaatgag	tagtccggag	cctaaaatta	actcatacgt	gaatttttaga	gatgaagttc	1260
ttcctcgcac	aaaaaagctt	gggtacaatg	cgtcgcaaat	tatggctatt	caagagcatt	1320
cttattatgc	tagtttttgt	tatcatgtca	caaatTTTTT	tgcaccaagc	agccgttttg	1380
gaacgcccga	cgaccttaag	tcttcgattg	ataaagctca	tgagctagga	attgttggtc	1440
tcattggacat	cgttcacagc	catgcatcaa	ataatacttt	agatggactg	aacatgtttg	1500
acggcaccga	tagttgttac	tttcaactctg	gagctcgtgg	ttatcattgg	atgtgggatt	1560
ccgcctcttt	aactatggaa	actgggaggt	acttaggtat	cttctctcaa	atgcgagatg	1620
gtgggttgat	gagttcaa	ttgatggatt	tagattcgat	ggtgtgacat	caatgatgta	1680
tactcaccac	ggattatcgg	tgggattcac	tgggaactac	gaggaatact	ttggactcgc	1740
aactgatgtg	gatgctgttg	tgtatctgat	gctggtcaac	gatcttattc	ataggctttt	1800

```

cccagatgca attaccattg gtgaagatgt tagcggaatg ccgacatttt gtattcccgt 1860
tcaagatggg ggtggtggct ttgactatcg gctgcatatg gcaattgctg ataaatggat 1920
tgagttgctc aagaaacggg atgaggattg gagagtgggt gatattgttc atacactgac 1980
aaatagaaga tggtcggaaa agtgtgtttc atacgctgaa agtcatgac aagctctagt 2040
cggtgataaa actatagcat tctggctgat ggacaaggat atgtatgatt ttatggctct 2100
ggatagaccg ccaacatcat taatagatcg tgggatagca ttgcacaaga tgattaggct 2160
tgtaactatg ggattaggag gagaagggtta cctaaatttc atgggaaatg aattcggcca 2220
ccctgagtgg attgatttcc ctagggtgta gccacacctt tctgatggct cagtaattcc 2280
cggaaaccaa ttcagttatg ataaatgcag acggagattt gacctgggag atgcagaata 2340
tttaagatac catgggttac aagaatttga ctgggctatg cagtatcttg aagataaata 2400
tgagtttatg acttcagaac accagttcat atcacgaaag gatgaaggag ataggatgat 2460
tgtatttgaa agaggaaacc tagttttcgt ctttaatttt cactggacaa atagctattc 2520
agactatcgc ataggctgcc tgaagcctgg aaaatacaag gttgtcttgg actcagatga 2580
tccacttttt ggtggcttcg ggagaattga tcataatgcc gaatatttca cctctgaagg 2640
atcgtatgat gatcgtcctt gttcaattat ggtgtatgca cctagtagaa cagcagtggg 2700
ctatgcacta gtagacaaac tagaagtagc agtagtagaa gaacccattg aagaatgaac 2760
gaacttgtga tcgcgttgaa agatttgaac gttacttggg catccacata gagcttcttg 2820
acatcagtct tggcggaatt gcatgtgaca acaaggtttg cagttctttc cactattagt 2880
agtccaccga tatacgcaga gatgaagtgc tgaacaaaca tatgtaaaat cgatgaattt 2940
atgtcgaatg ctgggacgat cgaattcctg cagcc 2975

```

```

<210> 14
<211> 3033
<212> DNA
<213> Solanum tuberosum

```

```

<220>
<221> CDS
<222> (96)..(116)

```

```

<220>
<221> CDS
<222> (145)..(2790)

```

```

<400> 14
ttgatggggc cttgaactca gcaatttgac actcagttag ttacactcct atcacttacc 60

```

```

agatctctat tttttctctt aattccaacc aagga atg aat aaa agg ata gat 113
Met Asn Lys Arg Ile Asp
1 5

```

```

ttg taaaaaccct aaggagagaa gaagaaag atg gtg tat aca ctc tct gga 165
Leu Met Val Tyr Thr Leu Ser Gly
10

```

```

gtt cgt ttt cct act gtt cca tca gtg tac aaa tct aat gga ttc agc 213
Val Arg Phe Pro Thr Val Pro Ser Val Tyr Lys Ser Asn Gly Phe Ser
15 20 25 30

```

```

agt aat ggt gat cgg agg aat gct aat gtt tct gta ttc ttg aaa aag 261
Ser Asn Gly Asp Arg Arg Asn Ala Asn Val Ser Val Phe Leu Lys Lys
35 40 45

```

cac tct ctt tca cgg aag atc ttg gct gaa aag tct tct tac aat tcc	309
His Ser Leu Ser Arg Lys Ile Leu Ala Glu Lys Ser Ser Tyr Asn Ser	
50 55 60	
gaa ttc cga cct tct aca gtt gca gca tcg ggg aaa gtc ctt gtg cct	357
Glu Phe Arg Pro Ser Thr Val Ala Ala Ser Gly Lys Val Leu Val Pro	
65 70 75	
gga acc cag agt gat agc tcc tca tcc tca aca gac caa ttt gag ttc	405
Gly Thr Gln Ser Asp Ser Ser Ser Ser Thr Asp Gln Phe Glu Phe	
80 85 90	
act gag aca tct cca gaa aat tcc cca gca tca act gat gta gat agt	453
Thr Glu Thr Ser Pro Glu Asn Ser Pro Ala Ser Thr Asp Val Asp Ser	
95 100 105 110	
tca aca atg gaa cac gct agc cag att aaa act gag aac gat gac gtt	501
Ser Thr Met Glu His Ala Ser Gln Ile Lys Thr Glu Asn Asp Asp Val	
115 120 125	
gag ccg tca agt gat ctt aca gga agt gtt gaa gag ctg gat ttt gct	549
Glu Pro Ser Ser Asp Leu Thr Gly Ser Val Glu Glu Leu Asp Phe Ala	
130 135 140	
tca tca cta caa cta caa gaa ggt ggt aaa ctg gag gag tct aaa aca	597
Ser Ser Leu Gln Leu Gln Glu Gly Gly Lys Leu Glu Glu Ser Lys Thr	
145 150 155	
tta aat act tct gaa gag aca att att gat gaa tct gat agg atc aga	645
Leu Asn Thr Ser Glu Glu Thr Ile Ile Asp Glu Ser Asp Arg Ile Arg	
160 165 170	
gag agg ggc atc cct cca cct gga ctt ggt cag aag att tat gaa ata	693
Glu Arg Gly Ile Pro Pro Pro Gly Leu Gly Gln Lys Ile Tyr Glu Ile	
175 180 185 190	
gac ccc ctt ttg aca aac tat cgt caa cac ctt gat tac agg tat tca	741
Asp Pro Leu Leu Thr Asn Tyr Arg Gln His Leu Asp Tyr Arg Tyr Ser	
195 200 205	
cag tac aag aaa ctg agg gag gca att gac aag tat gag ggt ggt ttg	789
Gln Tyr Lys Lys Leu Arg Glu Ala Ile Asp Lys Tyr Glu Gly Gly Leu	
210 215 220	
gaa gcc ttt tct cgt ggt tat gaa aaa atg ggt ttc act cgt agt gct	837
Glu Ala Phe Ser Arg Gly Tyr Glu Lys Met Gly Phe Thr Arg Ser Ala	
225 230 235	
aca ggt atc act tac cgt gag tgg gct ctt ggt gcc cag tca gct gcc	885
Thr Gly Ile Thr Tyr Arg Glu Trp Ala Leu Gly Ala Gln Ser Ala Ala	
240 245 250	

ctc att gga gat ttc aac aat tgg gac gca aat gct gac att atg act	933
Leu Ile Gly Asp Phe Asn Asn Trp Asp Ala Asn Ala Asp Ile Met Thr	
255 260 265 270	
cgg aat gaa ttt ggt gtc tgg gag att ttt ctg cca aat aat gtg gat	981
Arg Asn Glu Phe Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Val Asp	
275 280 285	
ggt tct cct gca att cct cat ggg tcc aga gtg aag ata cgt atg gac	1029
Gly Ser Pro Ala Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp	
290 295 300	
act cca tca ggt gtt aag gat tcc att cct gct tgg atc aac tac tct	1077
Thr Pro Ser Gly Val Lys Asp Ser Ile Pro Ala Trp Ile Asn Tyr Ser	
305 310 315	
tta cag ctt cct gat gaa att cca tat aat gga ata cat tat gat cca	1125
Leu Gln Leu Pro Asp Glu Ile Pro Tyr Asn Gly Ile His Tyr Asp Pro	
320 325 330	
ccc gaa gag gag agg tat atc ttc caa cac cca cgg cca aag aaa cca	1173
Pro Glu Glu Glu Arg Tyr Ile Phe Gln His Pro Arg Pro Lys Lys Pro	
335 340 345 350	
aag tcg ctg aga ata tat gaa tct cat att gga atg agt agt ccg gag	1221
Lys Ser Leu Arg Ile Tyr Glu Ser His Ile Gly Met Ser Ser Pro Glu	
355 360 365	
cct aaa att aac tca tac gtg aat ttt aga gat gaa gtt ctt cct cgc	1269
Pro Lys Ile Asn Ser Tyr Val Asn Phe Arg Asp Glu Val Leu Pro Arg	
370 375 380	
ata aaa aag ctt ggg tac aat gcg ctg caa att atg gct att caa gag	1317
Ile Lys Lys Leu Gly Tyr Asn Ala Leu Gln Ile Met Ala Ile Gln Glu	
385 390 395	
cat tct tat tac gct agt ttt ggt tat cat gtc aca aat ttt ttt gca	1365
His Ser Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala	
400 405 410	
cca agc agc cgt ttt gga acg ccc gac gac ctt aag tct ttg att gat	1413
Pro Ser Ser Arg Phe Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp	
415 420 425 430	
aaa gct cat gag cta gga att gtt gtt ctc atg gac att gtt cac agc	1461
Lys Ala His Glu Leu Gly Ile Val Val Leu Met Asp Ile Val His Ser	
435 440 445	
cat gca tca aat aat act tta gat gga ctg aac atg ttt gac tgc acc	1509
His Ala Ser Asn Asn Thr Leu Asp Gly Leu Asn Met Phe Asp Cys Thr	
450 455 460	



gat agt tgt tac ttt cac tct gga gct cgt ggt tat cat tgg atg tgg	1557
Asp Ser Cys Tyr Phe His Ser Gly Ala Arg Gly Tyr His Trp Met Trp	
465 470 475	
gat tcc cgc ctc ttt aac tat gga aac tgg gag gta ctt agg tat ctt	1605
Asp Ser Arg Leu Phe Asn Tyr Gly Asn Trp Glu Val Leu Arg Tyr Leu	
480 485 490	
ctc tca aat gcg aga tgg tgg ttg gat gcg ttc aaa ttt gat gga ttt	1653
Leu Ser Asn Ala Arg Trp Trp Leu Asp Ala Phe Lys Phe Asp Gly Phe	
495 500 505 510	
aga ttt gat ggt gtg aca tca atg atg tat att cac cac gga tta tcg	1701
Arg Phe Asp Gly Val Thr Ser Met Met Tyr Ile His His Gly Leu Ser	
515 520 525	
gtg gga ttc act ggg aac tac gag gaa tac ttt gga ctc gca act gat	1749
Val Gly Phe Thr Gly Asn Tyr Glu Glu Tyr Phe Gly Leu Ala Thr Asp	
530 535 540	
gtg gat gct gtt gtg tat ctg atg ctg gtc aac gat ctt att cat ggg	1797
Val Asp Ala Val Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly	
545 550 555	
ctt ttc cca gat gca att acc att ggt gaa gat gtt agc gga atg ccg	1845
Leu Phe Pro Asp Ala Ile Thr Ile Gly Glu Asp Val Ser Gly Met Pro	
560 565 570	
aca ttt tgt att ccc gtc caa gag ggg ggt gtt ggc ttt gac tat cgg	1893
Thr Phe Cys Ile Pro Val Gln Glu Gly Gly Val Gly Phe Asp Tyr Arg	
575 580 585 590	
ctg cat atg gca att gct gat aaa cgg att gag ttg ctc aag aaa cgg	1941
Leu His Met Ala Ile Ala Asp Lys Arg Ile Glu Leu Leu Lys Lys Arg	
595 600 605	
gat gag gat tgg aga gtg ggt gat att gtt cat aca ctg aca aat aga	1989
Asp Glu Asp Trp Arg Val Gly Asp Ile Val His Thr Leu Thr Asn Arg	
610 615 620	
aga tgg tcg gaa aag tgt gtt tca tac gct gaa agt cat gat caa gct	2037
Arg Trp Ser Glu Lys Cys Val Ser Tyr Ala Glu Ser His Asp Gln Ala	
625 630 635	
cta gtc ggt gat aaa act ata gca ttc tgg ctg atg gac aag gat atg	2085
Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met	
640 645 650	
tat gat ttt atg gct ctg gat aga ccg tca aca tca tta ata gat cgt	2133
Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Ser Leu Ile Asp Arg	
655 660 665 670	

ggg ata gca ttg cac aag atg att agg ctt gta act atg gga tta gga	2181
Gly Ile Ala Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly	
675 680 685	
gga gaa ggg tac cta aat ttc atg gga aat gaa ttc ggc cac cct gag	2229
Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu	
690 695 700	
tgg att gat ttc cct agg gct gaa caa cac ctc tct gat ggc tca gta	2277
Trp Ile Asp Phe Pro Arg Ala Glu Gln His Leu Ser Asp Gly Ser Val	
705 710 715	
atc ccc gga aac caa ttc agt tat gat aaa tgc aga cgg aga ttt gac	2325
Ile Pro Gly Asn Gln Phe Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp	
720 725 730	
ctg gga gat gca gaa tat tta aga tac cgt ggg ttg caa gaa ttt gac	2373
Leu Gly Asp Ala Glu Tyr Leu Arg Tyr Arg Gly Leu Gln Glu Phe Asp	
735 740 745 750	
cgg cct atg cag tat ctt gaa gat aaa tat gag ttt atg act tca gaa	2421
Arg Pro Met Gln Tyr Leu Glu Asp Lys Tyr Glu Phe Met Thr Ser Glu	
755 760 765	
cac cag ttc ata tca cga aag gat gaa gga gat agg atg att gta ttt	2469
His Gln Phe Ile Ser Arg Lys Asp Glu Gly Asp Arg Met Ile Val Phe	
770 775 780	
gaa aaa gga aac cta gtt ttt gtc ttt aat ttt cac tgg aca aaa agc	2517
Glu Lys Gly Asn Leu Val Phe Val Phe Asn Phe His Trp Thr Lys Ser	
785 790 795	
tat tca gac tat cgc ata gcc tgc ctg aag cct gga aaa tac aag gtt	2565
Tyr Ser Asp Tyr Arg Ile Ala Cys Leu Lys Pro Gly Lys Tyr Lys Val	
800 805 810	
gcc ttg gac tca gat gat cca ctt ttt ggt ggc ttc ggg aga att gat	2613
Ala Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly Phe Gly Arg Ile Asp	
815 820 825 830	
cat aat gcc gaa tat ttc acc ttt gaa gga tgg tat gat gat cgt cct	2661
His Asn Ala Glu Tyr Phe Thr Phe Glu Gly Trp Tyr Asp Asp Arg Pro	
835 840 845	
cgt tca att atg gtg tat gca cct tgt aaa aca gca gtg gtc tat gca	2709
Arg Ser Ile Met Val Tyr Ala Pro Cys Lys Thr Ala Val Val Tyr Ala	
850 855 860	
cta gta gac aaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gta	2757
Leu Val Asp Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Val	
865 870 875	

gca gca gta gaa gaa gta gta gta gaa gaa gaa tgaacgaact tgtgatcgcg 2810  
 Ala Ala Val Glu Glu Val Val Val Glu Glu Glu  
 880 885

ttgaaagatt tgaacgctac atagagcttc ttgacgtatc tggcaatatt gcatcagtct 2870

tggcggaatt tcatgtgaca caagggtttgc aattctttcc actattagta gtgcaacgat 2930

atacgcagag atgaagtgct gaacaaacat atgtaaaatc gatgaattta tgtcgaatgc 2990

tgggacgatc gaattcctgc aggcggggg accccttagt tct 3033

<210> 15

<211> 889

<212> PRT

<213> Solanum tuberosum

<400> 15

Met Asn Lys Arg Ile Asp Leu Met Val Tyr Thr Leu Ser Gly Val Arg  
 1 5 10 15

Phe Pro Thr Val Pro Ser Val Tyr Lys Ser Asn Gly Phe Ser Ser Asn  
 20 25 30

Gly Asp Arg Arg Asn Ala Asn Val Ser Val Phe Leu Lys Lys His Ser  
 35 40 45

Leu Ser Arg Lys Ile Leu Ala Glu Lys Ser Ser Tyr Asn Ser Glu Phe  
 50 55 60

Arg Pro Ser Thr Val Ala Ala Ser Gly Lys Val Leu Val Pro Gly Thr  
 65 70 75 80

Gln Ser Asp Ser Ser Ser Ser Thr Asp Gln Phe Glu Phe Thr Glu  
 85 90 95

Thr Ser Pro Glu Asn Ser Pro Ala Ser Thr Asp Val Asp Ser Ser Thr  
 100 105 110

Met Glu His Ala Ser Gln Ile Lys Thr Glu Asn Asp Asp Val Glu Pro  
 115 120 125

Ser Ser Asp Leu Thr Gly Ser Val Glu Glu Leu Asp Phe Ala Ser Ser  
 130 135 140

Leu Gln Leu Gln Glu Gly Gly Lys Leu Glu Glu Ser Lys Thr Leu Asn  
 145 150 155 160

Thr Ser Glu Glu Thr Ile Ile Asp Glu Ser Asp Arg Ile Arg Glu Arg  
 165 170 175

Gly Ile Pro Pro Pro Gly Leu Gly Gln Lys Ile Tyr Glu Ile Asp Pro  
 180 185 190

Leu	Leu	Thr	Asn	Tyr	Arg	Gln	His	Leu	Asp	Tyr	Arg	Tyr	Ser	Gln	Tyr	195	200	205	
Lys	Lys	Leu	Arg	Glu	Ala	Ile	Asp	Lys	Tyr	Glu	Gly	Gly	Leu	Glu	Ala	210	215	220	
Phe	Ser	Arg	Gly	Tyr	Glu	Lys	Met	Gly	Phe	Thr	Arg	Ser	Ala	Thr	Gly	225	230	235	240
Ile	Thr	Tyr	Arg	Glu	Trp	Ala	Leu	Gly	Ala	Gln	Ser	Ala	Ala	Leu	Ile	245	250	255	
Gly	Asp	Phe	Asn	Asn	Trp	Asp	Ala	Asn	Ala	Asp	Ile	Met	Thr	Arg	Asn	260	265	270	
Glu	Phe	Gly	Val	Trp	Glu	Ile	Phe	Leu	Pro	Asn	Asn	Val	Asp	Gly	Ser	275	280	285	
Pro	Ala	Ile	Pro	His	Gly	Ser	Arg	Val	Lys	Ile	Arg	Met	Asp	Thr	Pro	290	295	300	
Ser	Gly	Val	Lys	Asp	Ser	Ile	Pro	Ala	Trp	Ile	Asn	Tyr	Ser	Leu	Gln	305	310	315	320
Leu	Pro	Asp	Glu	Ile	Pro	Tyr	Asn	Gly	Ile	His	Tyr	Asp	Pro	Pro	Glu	325	330	335	
Glu	Glu	Arg	Tyr	Ile	Phe	Gln	His	Pro	Arg	Pro	Lys	Lys	Pro	Lys	Ser	340	345	350	
Leu	Arg	Ile	Tyr	Glu	Ser	His	Ile	Gly	Met	Ser	Ser	Pro	Glu	Pro	Lys	355	360	365	
Ile	Asn	Ser	Tyr	Val	Asn	Phe	Arg	Asp	Glu	Val	Leu	Pro	Arg	Ile	Lys	370	375	380	
Lys	Leu	Gly	Tyr	Asn	Ala	Leu	Gln	Ile	Met	Ala	Ile	Gln	Glu	His	Ser	385	390	395	400
Tyr	Tyr	Ala	Ser	Phe	Gly	Tyr	His	Val	Thr	Asn	Phe	Phe	Ala	Pro	Ser	405	410	415	
Ser	Arg	Phe	Gly	Thr	Pro	Asp	Asp	Leu	Lys	Ser	Leu	Ile	Asp	Lys	Ala	420	425	430	
His	Glu	Leu	Gly	Ile	Val	Val	Leu	Met	Asp	Ile	Val	His	Ser	His	Ala	435	440	445	
Ser	Asn	Asn	Thr	Leu	Asp	Gly	Leu	Asn	Met	Phe	Asp	Cys	Thr	Asp	Ser	450	455	460	
Cys	Tyr	Phe	His	Ser	Gly	Ala	Arg	Gly	Tyr	His	Trp	Met	Trp	Asp	Ser	465	470	475	480

Arg	Leu	Phe	Asn	Tyr	Gly	Asn	Trp	Glu	Val	Leu	Arg	Tyr	Leu	Leu	Ser	485	490	495
Asn	Ala	Arg	Trp	Trp	Leu	Asp	Ala	Phe	Lys	Phe	Asp	Gly	Phe	Arg	Phe	500	505	510
Asp	Gly	Val	Thr	Ser	Met	Met	Tyr	Ile	His	His	Gly	Leu	Ser	Val	Gly	515	520	525
Phe	Thr	Gly	Asn	Tyr	Glu	Glu	Tyr	Phe	Gly	Leu	Ala	Thr	Asp	Val	Asp	530	535	540
Ala	Val	Val	Tyr	Leu	Met	Leu	Val	Asn	Asp	Leu	Ile	His	Gly	Leu	Phe	545	550	555
Pro	Asp	Ala	Ile	Thr	Ile	Gly	Glu	Asp	Val	Ser	Gly	Met	Pro	Thr	Phe	565	570	575
Cys	Ile	Pro	Val	Gln	Glu	Gly	Gly	Val	Gly	Phe	Asp	Tyr	Arg	Leu	His	580	585	590
Met	Ala	Ile	Ala	Asp	Lys	Arg	Ile	Glu	Leu	Leu	Lys	Lys	Arg	Asp	Glu	595	600	605
Asp	Trp	Arg	Val	Gly	Asp	Ile	Val	His	Thr	Leu	Thr	Asn	Arg	Arg	Trp	610	615	620
Ser	Glu	Lys	Cys	Val	Ser	Tyr	Ala	Glu	Ser	His	Asp	Gln	Ala	Leu	Val	625	630	635
Gly	Asp	Lys	Thr	Ile	Ala	Phe	Trp	Leu	Met	Asp	Lys	Asp	Met	Tyr	Asp	645	650	655
Phe	Met	Ala	Leu	Asp	Arg	Pro	Ser	Thr	Ser	Leu	Ile	Asp	Arg	Gly	Ile	660	665	670
Ala	Leu	His	Lys	Met	Ile	Arg	Leu	Val	Thr	Met	Gly	Leu	Gly	Gly	Glu	675	680	685
Gly	Tyr	Leu	Asn	Phe	Met	Gly	Asn	Glu	Phe	Gly	His	Pro	Glu	Trp	Ile	690	695	700
Asp	Phe	Pro	Arg	Ala	Glu	Gln	His	Leu	Ser	Asp	Gly	Ser	Val	Ile	Pro	705	710	715
Gly	Asn	Gln	Phe	Ser	Tyr	Asp	Lys	Cys	Arg	Arg	Arg	Phe	Asp	Leu	Gly	725	730	735
Asp	Ala	Glu	Tyr	Leu	Arg	Tyr	Arg	Gly	Leu	Gln	Glu	Phe	Asp	Arg	Pro	740	745	750
Met	Gln	Tyr	Leu	Glu	Asp	Lys	Tyr	Glu	Phe	Met	Thr	Ser	Glu	His	Gln	755	760	765

Phe Ile Ser Arg Lys Asp Glu Gly Asp Arg Met Ile Val Phe Glu Lys  
 770 775 780  
 Gly Asn Leu Val Phe Val Phe Asn Phe His Trp Thr Lys Ser Tyr Ser  
 785 790 795 800  
 Asp Tyr Arg Ile Ala Cys Leu Lys Pro Gly Lys Tyr Lys Val Ala Leu  
 805 810 815  
 Asp Ser Asp Asp Pro Leu Phe Gly Gly Phe Gly Arg Ile Asp His Asn  
 820 825 830  
 Ala Glu Tyr Phe Thr Phe Glu Gly Trp Tyr Asp Asp Arg Pro Arg Ser  
 835 840 845  
 Ile Met Val Tyr Ala Pro Cys Lys Thr Ala Val Val Tyr Ala Leu Val  
 850 855 860  
 Asp Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Val Ala Ala  
 865 870 875 880  
 Val Glu Glu Val Val Val Glu Glu Glu  
 885

<210> 16

<211> 2576

<212> DNA

<213> Solanum tuberosum

<400> 16

tcattaaaga	ggagaaatta	actatgagag	gatctcacca	tcaccatcac	catgggatct	60
tggttgaaaa	gtcttcttac	aattccgaat	tccgaccttc	tacagttgca	gcatcgggga	120
aagtccttgt	gcctggaacc	cagagtgata	gctcctcatc	ctcaacaaac	caatttgagt	180
tactgagac	atctccagaa	aattccccag	catcaactga	tgtagatagt	tcaacaatgg	240
aacacgctag	ccagattaaa	actgagaacg	atgacgttga	gccgtcaagt	gatcttacag	300
gaagtgttga	agagctggat	tttgcttcat	cactacaact	acaagaagg	ggtaaactgg	360
aggagtctaa	aacattaaat	acttctgaag	agacaattat	tgatgaatct	gataggatca	420
gagagagggg	catccctcca	cctggacttg	gtcagaagat	ttatgaaata	gacccctttt	480
tgacaaacta	tcgtcaacac	cttgattaca	ggtattcaca	gtacaagaaa	ctgagggagg	540
caattgacaa	gtatgagggt	ggtttggaag	ctttttctcg	tggttatgaa	aaaatggggt	600
tcactcgtag	tgctacaggt	atcacttacc	gtgagtgggc	tcctggtgcc	cagtcagctg	660
ccctcattgg	agatttcaac	aattgggacg	caaatgctga	cattatgact	cggaatgaat	720
ttggtgtctg	ggagattttt	ctgccaaata	atgtggatgg	ttctcctgca	attcctcatg	780
ggtccagagt	gaagatacgt	atggacactc	catcaggtgt	taaggattcc	attcctgctt	840
ggatcaacta	ctctacagct	tcctgatgaa	attccatata	atggaatata	ttatgatcca	900
cccgaagagg	agaggtatat	cttccaacac	ccacggccaa	agaaaccaa	gtcgtgaga	960
atatatgaat	ctcatattgg	aatgagtagt	cgggagccta	aaattaactc	atacgtgaat	1020
tttagagatg	aagttcttcc	tcgcataaaa	aagcttgggg	acaatgcgct	gcaaattatg	1080
gctattcaag	agcattctta	ttatgctagt	tttggttatc	atgtcacaaa	tttttttgca	1140
ccaagcagcc	gttttggaac	gcccagcgac	cttaagtctt	tgattgataa	agctcatgag	1200
ctaggaattg	ttgttctcat	ggacattggt	cacagccatg	catcaaataa	tacttttagat	1260
ggactgaaca	tgtttgacgg	caccgatagt	tgttactttc	actctggagc	tcgtgggttat	1320

cattggatgt	gggattcccc	cctttttaac	tatggaaact	gggagggtact	taggtatctt	1380
ctctcaaatg	cgagatgggtg	gttggatgag	ttcaaatttg	atggatttag	atttgatggt	1440
gtgacatcaa	tgatgtatac	tcaccacgga	ttatcgggtg	gattcactgg	gaactacgag	1500
gaatactttg	gactcgcaac	tgatgtggat	gctgttgtgt	atctgatgct	ggtcaacgat	1560
cttattcatg	ggcttttccc	agatgcaatt	accattgggtg	aagatgttag	cggaatgccg	1620
acattttgta	ttcccgttca	agatgggggt	gttggctttg	actatcggct	gcatatggca	1680
attgctgata	aatggattga	gttgctcaag	aaacgggatg	aggattggag	agtgggtgat	1740
attgttcata	cactgacaaa	tagaagatgg	tcggaaaagt	gtgtttcata	cgctgaaagt	1800
catgatcaag	ctctagtcgg	tgataaaact	atagcattct	ggctgatgga	caaggatatg	1860
tatgatttta	tggctctgga	tagaccgcca	acatcattaa	tagatcgtgg	gatagcattg	1920
cacaagatga	ttaggcttgt	aactatggga	ttaggaggag	aaggggtacct	aaatttcatg	1980
ggaaatgaat	tcggccaccc	tgagtggatt	gattttcccta	gggctgaaca	acacctctct	2040
gatgactcag	taattccccg	aaaccaattc	agttatgata	aatgcagacg	gagatttgac	2100
ctgggagatg	cagaatattt	aagataccgt	gggttgcaag	aatttgaccg	ggctatgcag	2160
tatcttgaag	ataaatatga	gtttatgact	tcagaacacc	agttcatatc	acgaaaggat	2220
gaaggagata	ggatgattgt	atttgaaaaa	ggaaacctag	tttttgtctt	taattttcac	2280
tggacaaaaa	gctattcaga	ctatcgcata	ggctgcctga	agcctggaaa	atacaagggt	2340
gccttggaat	cagatgatcc	actttttggt	ggcttcggga	gaattgatca	taatgccgaa	2400
tatttcacct	ttgaaggatg	gtatgatgat	cgcttcggtt	caattatggt	gtatgcacct	2460
tgtagaacag	cagtgggtcta	tgactagtag	gacaaagaag	aagaagaaga	agaagaagaa	2520
gaagaagtag	cagtagtaga	agaagtagta	gtagaagaag	aatgaacgaa	cttgtg	2576

<210> 17

<211> 2529

<212> DNA

<213> Solanum tuberosum

<220>

<221> modified\_base

<222> (2492)..(2492)

<223> a, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (2499)..(2499)

<223> a, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (2516)..(2516)

<223> a, c, g, t, other or unknown

<220>

<221> modified\_base

<222> (2520)..(2521)

<223> a, c, g, t, other or unknown

<400> 17

ggatgcta	atgtttct	gtatcttt	tgaaaaa	gcactctctt	tcacggaaga	tcttggtg	ta	60
aaagtctt	cttaca	atttcc	cgacct	ttctacag	ttgcagcat	cggtgaa	agtcct	120
tgtgcctg	gaaycc	agagtg	atagctc	ctcctca	acagacca	attttg	agttcact	180
gacatctc	ccagaaa	atttccc	cagcatca	acatgat	gtatgtag	atgttca	acacgc	240
tagccagat	taaaact	tgacac	gctgtg	agccgtca	agtgatct	taaggaa	agtgt	300

tgaagagctg	gatttttgc	catcactaca	actacaagaa	ggtggtaa	tggaggagtc	360
taaaacatta	aatacttctg	aagagacaat	tattgatgaa	tctgatagga	tcagagagag	420
gggcatccct	ccacctggac	ttggtcagaa	gatttatgaa	atagaccccc	ttttgacaaa	480
ctatcgtaaa	caccttgatt	acaggtattc	acagtacaag	aaactgaggg	aggcaattga	540
caagtatgag	ggtggtttg	aagctttttc	tcgtggttat	gaaaaaatgg	gtttcactcg	600
tagtgctaca	ggtatcactt	accgtgagtg	ggctcctgg	gcccagtcag	ctgccctcat	660
tggagatttc	aacaattggg	acgcaa	tgacattatg	actcggaatg	aatttgggtg	720
ctgggagatt	tttctgccaa	ataatgtgga	tggttctcct	gcaattcctc	atgggtccag	780
agtgaagata	cgyatggaca	ctccatcagg	tgtaaggat	tccattcctg	cttggatcaa	840
ctactcttta	cagcttctctg	atgaaattcc	atataatgga	atatattatg	atccaccga	900
aggagagagg	tatrtcttcc	aacaccacg	gccaagaaa	ccaaagtcgc	tgagaatata	960
tgaatctcat	attggaatga	gtagtcgga	gcctaaaatt	aactcatacg	tgaatttttag	1020
agatgaagtt	cttctctgca	taaaaaasct	tgggtacaat	gcggtgcaaa	ttatggctat	1080
tcaagagcat	tcttattatg	ctagtttttg	ttatcatgtc	acaaattttt	ttgcaccaag	1140
cagccgtttt	ggaacgccc	acgaccttaa	gtctttgatt	gataaagctc	atgagctagg	1200
aattgttggt	ctcatggaca	ttgttcacag	ccatgcatca	aataatactt	tagatggact	1260
gaacatggtt	gacggcacag	atagttgtta	ctttcactct	ggagctcgtg	gttatcattg	1320
gatgtgggat	tcccgcctct	ttaactatgg	aaactgggag	gtacttaggt	atcttctctc	1380
aaatgcgaga	tggtggttg	atgagttcaa	atttgatgga	tttagatttg	atgggtgtgac	1440
atcaatgatg	tatactcacc	acggattatc	ggtgggattc	actgggaact	acgaggaata	1500
ctttgggact	gcaactgatg	tggtatgctg	tggtatctg	atgctggtca	acgatcttat	1560
tcacgggctt	ttcccagatg	caattaccat	tggtgaagat	gttagcggaa	tgccgacatt	1620
ttgtattccc	gttcaagatg	ggggtgttg	ctttgactat	cggctgcata	tggcaattgc	1680
tgataaatgg	attgagttgc	tcaagaaacg	ggatgaggat	tggagagtgg	gtgatattgt	1740
tcatacactg	acaaatagaa	gatggtcgga	aaagtgtgtt	tcatmcgctg	aaagtcatga	1800
tcaagctcta	gtcggtgata	aaactatagc	atytctggctg	atggacaagg	atatgtatga	1860
ttttatggct	ctggatagac	cgycaacayc	attaatagat	cgtgggatag	cattgcacaa	1920
gatgattagg	cttgtaacta	tgggattagg	aggagaaggg	tacctaaatt	tcatgggaaa	1980
tgaattcggc	caccctgagt	ggattgattt	ccctagggct	garcaacacc	tctctgatgg	2040
ctcagtaatt	cccggaaacc	aattcagtta	tgataaatgc	agacggagat	ttgacctggg	2100
agatgcagaa	tatttaagat	accatgggtt	gcaagaattt	gaccgggcta	tgcagtatct	2160
tgaagataaa	tatgagttta	tgacttcaga	acaccagttc	atatcacgaa	aggatgaagg	2220
agataggatg	attgtatttg	aaaraggaaa	cctagttttt	gtctttaatt	ttcactggac	2280
aaatagctat	tcagactatc	gcataggctg	cctgaagcct	ggaaaataca	aggttggtct	2340
ggactcagat	gatccacttt	ttggtggctt	cgggagaatt	gatcataatg	ccgaatattt	2400
cacctctgaa	ggatcgatg	atgatcgctc	tcgttcaatt	atgggtgtatg	cacctagtag	2460
aacagcagtg	gtctatgcac	tagtagacaa	antagaagna	gaagaagaag	aagaanccgn	2520
ngaagaatt						2529

&lt;210&gt; 18

&lt;211&gt; 3187

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (3071)..(3071)

&lt;223&gt; a, c, g, t, other or unknown

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (3159)..(3159)

&lt;223&gt; a, c, g, t, other or unknown



<220>  
 <221> modified\_base  
 <222> (3162)..(3165)  
 <223> a, c, g, t, other or unknown

<400> 18  
 aaaaacctcc tccactcagt cttgggatct ctctctctct tcacgcttct cttggggcct 60  
 tgaactcagc aatttgacac tcagttagtt acactgccat cactcatcag atctctattt 120  
 tttctcttaa ttccaaccaa ggaatgaatt aaaagattag atttgaagga gagaagaaga 180  
 aagatggtgt atacactctc tggagttcgt tttcctactg ttccatcagt gtacaaatct 240  
 aatggattca gcagtaatgg tgatcggagg aatgctaattg tttctgtatt cttgaaaaag 300  
 cactctcttt cacggaagat cttggctgaa aagtcttctt acgattccga atcccgacct 360  
 tctacagttg cagcatcggg gaaagtcctt gtacctggaa tccagagtga tagctcctca 420  
 tcctcaacag accaatttga gttcactgag acagctccag aaaattcccc agcatcaact 480  
 gatgtggata gttcaacaat ggaacacgct agccagatta aaactgagaa cgatgacgtt 540  
 gagccgtcaa gtgatcttac aggaagtgtt gaagagttgg attttgcttc atcactacaa 600  
 ctacaagaag gtggtaaact ggaggagtct aaaacattaa atacttctga agagacaaat 660  
 attgatgaat ctgataggat cagagagagg ggcattccctc cacttggaag tggtcagaag 720  
 atttatgaaa tagaccctt tttgacaaac tatcgtcaac accttgatta caggtattca 780  
 cagtacaaga aaatgagggg ggcaattgac aagtatgagg gtggttttga agctttttct 840  
 cgtggttatg aaaaaatggg tttcactcgt agtgctacag gtatcactta ccgtgagtgg 900  
 gctcctggtg ccagtcagc tgctctcatt ggagatttca acaattggga cgcaaagtct 960  
 gacattatga ctcggaatga atttggtgtc tgggagattt ttctgccaaa taatgtggat 1020  
 ggttctcctg caattcctca tgggtccaga gtgaagatac gcatggacac ttcacaggt 1080  
 gttaaggatt ccattcctgc ttgatcaac tactctttac agcttctctga tgaaattcca 1140  
 tataatggaa tatattatga tccaccgaa gaggagaggt atgtcttcca acaccacgg 1200  
 ccaaagaaac caaagtcgct gagaatatat gaatctcata ttggaatgag tagtccggag 1260  
 cctaaaatta actcatcagt gaattttaga gatgaagttc ttctcgcac aaaaaacctt 1320  
 ggggtacaatg cggtgcaaat tatggctatt caagagcatt cttattatgc tagttttggt 1380  
 tatcatgtca caaatttttt tgcaccaagc agccgttttg gaacgcccga cgaccttaag 1440  
 tctttgattg ataaagctca tgagctagga attgttggtc tcatggacat tgttcacagc 1500  
 catgcatcaa ataatacttt agatggactg aacatgtttg acggcacaga tagttgttac 1560  
 tttcactctg gagctcgtgg ttatcattgg atgtgggatt cccgcctctt taactatgga 1620  
 aactgggagg tacttaggta tcttctctca aatgcgagat ggtggttga tgagtgcmaa 1680  
 tttgrtggtt ttagattcga tgggtgtgaca tcaatgatgt atactacca cggattatcg 1740  
 gtgggattca ctgggaacta cgaggaatac tttggactcg caactgatgt rgatgtgcc 1800  
 gtgtatctga tgctggccaa cgatcttatt catgggcttt tcccagatgc aattaccatt 1860  
 ggtgaagatg ttagcggaat gccgacattt tgtattcccg ttcaagatgg ggggtgttggc 1920  
 tttgactatc ggctgcata ggcaattgct gataaatgga ttgagttgct caagaaacgg 1980  
 gatgaggatt ggagagtggg tgatattggt catacactga caaatagaag atggctcgaa 2040  
 aagtgtgttt catacgctga aagtcatgat caagctctag tcggtgataa aactatagca 2100  
 ttctggctga tggacaagga tatgtatgat tttatggctt tggatagacc gtcaacatca 2160  
 ttaatagatc gtgggatatg attgcacaag atgattagga ttgtaactat gggattagga 2220  
 ggagaagggt acctaaattt catgggaaat gaattcggcc accctgagtg gattgatttc 2280  
 cctagggtcg aacaacacct ctctgatggc tcagtaattc ccggaacca attcagttat 2340  
 gataaatgca gacggagatt tgacctggga gatgcagaat atttaagata ccgtgggttg 2400  
 caagaatttg accgggctat gcagtatctt gaagataaat atgagtttat gacttcagaa 2460  
 caccagttca tatcacgaaa ggatgaagga gataggatga ttgtatttga aaaaggaaac 2520  
 ctagtttttg tctttaattt tcaactggga aaaagctatt cagactatcg cataggctgg 2580  
 ctgaagcctg gaaaatacaa ggttgccctg gactcagatg atccactttt tgggtggcttc 2640  
 gggagaattg atcataatgc cgaatgtttc acctttgaag gatggtatga tgatcgtcct 2700  
 cgttcaatta tgggtgatgc acctagtaga acagcagtggt tctatgcact agtagacaaa 2760  
 gaagaagaag aagaagaagt agcagtagta gaagaagtag tagtagaaga agaataaacg 2820

aacttgatgat	cgcgttgaaa	gatttgaacg	ctacatagag	cttcttgacg	tatctggcaa	2880
tattgcatca	gtcttggcgg	aatttcatgt	gacaaaaggt	ttgcaattct	ttccactatt	2940
agtagtgcaa	cgatatacgc	agagatgaag	tgctgaacaa	acatatgtaa	aatcgatgaa	3000
tttatgtcga	atgctgggac	gggcttcagc	aggttttgct	tagtgagttc	tgtaaattgt	3060
catctcttta	natgtacagc	ccactagaaa	tcaattatgt	gagacctaaa	aaacaataac	3120
cataaaattg	aaatagtgtc	gatctaata	tggtttaanc	cnnnnaaaaa	aaaaaaaaaa	3180
actcgag						3187

```
<210> 19
<211> 2578
<212> DNA
<213> Solanum tuberosum
```

```
<220>  
<221> CDS  
<222> (24) .. (2564)
```

```
<400> 19
tcattaaaga ggagaaatta act atg aga gga tct cac cat cac cat cac cat      53
                        Met Arg Gly Ser His His His His His His
                        1          5          10
```

ggg atc ttg gct gaa aag tct tct tac aat tcc gaa ttc cga cct tct 101  
Gly Ile Leu Ala Glu Lys Ser Ser Tyr Asn Ser Glu Phe Arg Pro Ser  
15 20 25

aca gtt gca gca tcg ggg aaa gtc ctt gtg cct gga acc cag agt gat 149  
Thr Val Ala Ala Ser Gly Lys Val Leu Val Pro Gly Thr Gln Ser Asp  
30 35 40

agc tcc tca tcc tca aca aac caa ttt gag ttc act gag aca tct cca 197  
 Ser Ser Ser Ser Ser Thr Asn Gln Phe Glu Phe Thr Glu Thr Ser Pro  
 45 50 55

gaa aat tcc cca gca tca act gat gta gat agt tca aca atg gaa cac 245  
Glu Asn Ser Pro Ala Ser Thr Asp Val Asp Ser Ser Thr Met Glu His  
60 65 70

gct agc cag att aaa act gag aac gat gac gtt gag ccg tca agt gat 293  
Ala Ser Gln Ile Lys Thr Glu Asn Asp Asp Val Glu Pro Ser Ser Asp  
75 80 85 90

ctt aca gga agt gtt gaa gag ctg gat ttt gct tca tca cta caa cta 341  
 Leu Thr Gly Ser Val Glu Glu Leu Asp Phe Ala Ser Ser Leu Gln Leu  
 95 100 105

caa gaa ggt ggt aaa ctg gag gag tct aaa aca tta aat act tct gaa 389  
Gln Glu Gly Gly Lys Leu Glu Glu Ser Lys Thr Leu Asn Thr Ser Glu  
110 115 120

gag aca att att gat gaa tct gat agg atc aga gag agg ggc atc cct 437  
Glu Thr Ile Ile Asp Glu Ser Asp Arg Ile Arg Glu Arg Gly Ile Pro  
125 130 135

cca cct gga ctt ggt cag aag att tat gaa ata gac ccc ctt ttg aca	485
Pro Pro Gly Leu Gly Gln Lys Ile Tyr Glu Ile Asp Pro Leu Leu Thr	
140 145 150	
aac tat cgt caa cac ctt gat tac agg tat tca cag tac aag aaa ctg	533
Asn Tyr Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Lys Leu	
155 160 165 170	
agg gag gca att gac aag tat gag ggt ggt ttg gaa gct ttt tct cgt	581
Arg Glu Ala Ile Asp Lys Tyr Glu Gly Gly Leu Glu Ala Phe Ser Arg	
175 180 185	
ggt tat gaa aaa atg ggt ttc act cgt agt gct aca ggt atc act tac	629
Gly Tyr Glu Lys Met Gly Phe Thr Arg Ser Ala Thr Gly Ile Thr Tyr	
190 195 200	
cgt gag tgg gct cct ggt gcc cag tca gct gcc ctc att gga gat ttc	677
Arg Glu Trp Ala Pro Gly Ala Gln Ser Ala Ala Leu Ile Gly Asp Phe	
205 210 215	
aac aat tgg gac gca aat gct gac att atg act cgg aat gaa ttt ggt	725
Asn Asn Trp Asp Ala Asn Ala Asp Ile Met Thr Arg Asn Glu Phe Gly	
220 225 230	
gtc tgg gag att ttt ctg cca aat aat gtg gat ggt tct cct gca att	773
Val Trp Glu Ile Phe Leu Pro Asn Asn Val Asp Gly Ser Pro Ala Ile	
235 240 245 250	
cct cat ggg tcc aga gtg aag ata cgt atg gac act cca tca ggt gtt	821
Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Val	
255 260 265	
aag gat tcc att cct gct tgg atc aac tac tct tca cag ctt cct gat	869
Lys Asp Ser Ile Pro Ala Trp Ile Asn Tyr Ser Ser Gln Leu Pro Asp	
270 275 280	
gaa att cca tat aat gga ata tat tat gat cca ccc gaa gag gag agg	917
Glu Ile Pro Tyr Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Arg	
285 290 295	
tat atc ttc caa cac cca cgg cca aag aaa cca aag tcg ctg aga ata	965
Tyr Ile Phe Gln His Pro Arg Pro Lys Lys Pro Lys Ser Leu Arg Ile	
300 305 310	
tat gaa tct cat att gga atg agt agt ccg gag cct aaa att aac tca	1013
Tyr Glu Ser His Ile Gly Met Ser Ser Pro Glu Pro Lys Ile Asn Ser	
315 320 325 330	
tac gtg aat ttt aga gat gaa gtt ctt cct cgc ata aaa aag ctt ggg	1061
Tyr Val Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Lys Leu Gly	
335 340 345	

tac aat gcg gtg caa att atg gct att caa gag cat tct tat tat gct	1109
Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala	
350 355 360	
agt ttt ggt tat cat gtc aca aat ttt ttt gca cca agc agc cgt ttt	1157
Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe	
365 370 375	
gga acg ccc gac gac ctt aag tct ttg att gat aaa gct cat gag cta	1205
Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu	
380 385 390	
gga att gtt gtt ctc atg gac att gtt cac agc cat gca tca aat aat	1253
Gly Ile Val Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn	
395 400 405 410	
act tta gat gga ctg aac atg ttt gac ggc acc gat agt tgt tac ttt	1301
Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe	
415 420 425	
cac tct gga gct cgt ggt tat cat tgg atg tgg gat tcc cgc ctt ttt	1349
His Ser Gly Ala Arg Gly Tyr His Trp Met Trp Asp Ser Arg Leu Phe	
430 435 440	
aac tat gga aac tgg gag gta ctt agg tat ctt ctc tca aat gcg aga	1397
Asn Tyr Gly Asn Trp Glu Val Leu Arg Tyr Leu Leu Ser Asn Ala Arg	
445 450 455	
tgg tgg ttg gat gag ttc aaa ttt gat gga ttt aga ttt gat ggt gtg	1445
Trp Trp Leu Asp Glu Phe Lys Phe Asp Gly Phe Arg Phe Asp Gly Val	
460 465 470	
aca tca atg atg tat act cac cac gga tta tcg gtg gga ttc act ggg	1493
Thr Ser Met Met Tyr Thr His His Gly Leu Ser Val Gly Phe Thr Gly	
475 480 485 490	
aac tac gag gaa tac ttt gga ctc gca act gat gtg gat gct gtt gtg	1541
Asn Tyr Glu Glu Tyr Phe Gly Leu Ala Thr Asp Val Asp Ala Val Val	
495 500 505	
tat ctg atg ctg gtc aac gat ctt att cat ggg ctt ttc cca gat gca	1589
Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu Phe Pro Asp Ala	
510 515 520	
att acc att ggt gaa gat gtt agc gga atg ccg aca ttt tgt att ccc	1637
Ile Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Cys Ile Pro	
525 530 535	
gtt caa gat ggg ggt gtt ggc ttt gac tat cgg ctg cat atg gca att	1685
Val Gln Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile	
540 545 550	

gct gat aaa tgg att gag ttg ctc aag aaa cgg gat gag gat tgg aga Ala Asp Lys Trp Ile Glu Leu Leu Lys Lys Arg Asp Glu Asp Trp Arg 555 560 565 570	1733
gtg ggt gat att gtt cat aca ctg aca aat aga aga tgg tcg gaa aag Val Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Ser Glu Lys 575 580 585	1781
tgt gtt tca tac gct gaa agt cat gat caa gct cta gtc ggt gat aaa Cys Val Ser Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys 590 595 600	1829
act ata gca ttc tgg ctg atg gac aag gat atg tat gat ttt atg gct Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala 605 610 615	1877
ctg gat aga ccg cca aca tca tta ata gat cgt ggg ata gca ttg cac Leu Asp Arg Pro Pro Thr Ser Leu Ile Asp Arg Gly Ile Ala Leu His 620 625 630	1925
aag atg att agg ctt gta act atg gga tta gga gga gaa ggg tac cta Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu 635 640 645 650	1973
aat ttc atg gga aat gaa ttc ggc cac cct gag tgg att gat ttc cct Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro 655 660 665	2021
agg gct gaa caa cac ctc tct gat gac tca gta att ccc gga aac caa Arg Ala Glu Gln His Leu Ser Asp Asp Ser Val Ile Pro Gly Asn Gln 670 675 680	2069
ttc agt tat gat aaa tgc aga cgg aga ttt gac ctg gga gat gca gaa Phe Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Glu 685 690 695	2117
tat tta aga tac cgt ggg ttg caa gaa ttt gac cgg gct atg cag tat Tyr Leu Arg Tyr Arg Gly Leu Gln Glu Phe Asp Arg Ala Met Gln Tyr 700 705 710	2165
ctt gaa gat aaa tat gag ttt atg act tca gaa cac cag ttc ata tca Leu Glu Asp Lys Tyr Glu Phe Met Thr Ser Glu His Gln Phe Ile Ser 715 720 725 730	2213
cga aag gat gaa gga gat agg atg att gta ttt gaa aaa gga aac cta Arg Lys Asp Glu Gly Asp Arg Met Ile Val Phe Glu Lys Gly Asn Leu 735 740 745	2261
gtt ttt gtc ttt aat ttt cac tgg aca aaa agc tat tca gac tat cgc Val Phe Val Phe Asn Phe His Trp Thr Lys Ser Tyr Ser Asp Tyr Arg 750 755 760	2309

ata ggc tgc ctg aag cct gga aaa tac aag gtt gcc ttg gac tca gat 2357  
 Ile Gly Cys Leu Lys Pro Gly Lys Tyr Lys Val Ala Leu Asp Ser Asp  
 765 770 775  
  
 gat cca ctt ttt ggt ggc ttc ggg aga att gat cat aat gcc gaa tat 2405  
 Asp Pro Leu Phe Gly Gly Phe Gly Arg Ile Asp His Asn Ala Glu Tyr  
 780 785 790  
  
 ttc acc ttt gaa gga tgg tat gat gat cgt cct cgt tca att atg gtg 2453  
 Phe Thr Phe Glu Gly Trp Tyr Asp Asp Arg Pro Arg Ser Ile Met Val  
 795 800 805 810  
  
 tat gca cct tgt aga aca gca gtg gtc tat gca cta gta gac aaa gaa 2501  
 Tyr Ala Pro Cys Arg Thr Ala Val Val Tyr Ala Leu Val Asp Lys Glu  
 815 820 825  
  
 gaa gaa gaa gaa gaa gaa gaa gaa gaa gta gca gta gta gaa gaa gta 2549  
 Glu Glu Glu Glu Glu Glu Glu Glu Glu Val Ala Val Val Glu Glu Val  
 830 835 840  
  
 gta gta gaa gaa gaa tgaacgaact tgtg 2578  
 Val Val Glu Glu Glu  
 845

<210> 20  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<220>  
 <221> modified\_base  
 <222> (12)..(12)  
 <223> inosine

<400> 20  
 aatttyatgg gnaaygartt ygg

23

<210> 21  
 <211> 203  
 <212> PRT  
 <213> Zea mays

<400> 21  
 Pro Ser Thr Pro Thr Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile  
 1 5 10 15  
  
 Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met  
 20 25 30

Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Pro  
           35                                  40                                  45  
 Gln Arg Leu Pro Ser Gly Lys Phe Ile Pro Gly Asn Asn Asn Ser Tyr  
           50                                  55                                  60  
 Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg  
   65                                  70                                  75                                  80  
 Tyr His Gly Met Gln Glu Phe Asp Gln Ala Met Gln His Leu Glu Gln  
                                   85                                  90                                  95  
 Lys Tyr Glu Phe Met Thr Ser Asp His Gln Tyr Ile Ser Arg Lys His  
                                   100                                  105                                  110  
 Glu Glu Asp Lys Val Ile Val Phe Glu Lys Gly Asp Leu Val Phe Val  
           115                                  120                                  125  
 Phe Asn Phe His Cys Asn Asn Ser Tyr Phe Asp Tyr Arg Ile Gly Cys  
           130                                  135                                  140  
 Arg Lys Pro Gly Val Tyr Lys Val Val Leu Asp Ser Asp Ala Gly Leu  
   145                                  150                                  155                                  160  
 Phe Gly Gly Phe Ser Arg Ile His His Ala Ala Glu His Phe Thr Ala  
                                   165                                  170                                  175  
 Asp Cys Ser His Asp Asn Arg Pro Tyr Ser Phe Ser Val Tyr Thr Pro  
           180                                  185                                  190  
 Ser Arg Thr Cys Val Val Tyr Ala Pro Val Glu  
           195                                  200

<210> 22  
 <211> 213  
 <212> PRT  
 <213> Lathyrus sp.

<400> 22  
 Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile  
   1                                  5                                  10                                  15  
 Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met  
           20                                  25                                  30  
 Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Gly Glu  
           35                                  40                                  45  
 Gln His Leu Pro Asn Gly Lys Ile Val Pro Gly Asn Asn Asn Ser Tyr  
           50                                  55                                  60

Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp Tyr Leu Arg  
 65 70 75 80  
 Tyr His Gly Met Gln Glu Phe Asp Arg Ala Met Gln His Leu Glu Glu  
 85 90 95  
 Thr Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser Arg Lys Asn  
 100 105 110  
 Glu Gly Asp Arg Val Ile Ile Phe Glu Arg Asp Asn Leu Val Phe Val  
 115 120 125  
 Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Lys Val Gly Cys  
 130 135 140  
 Leu Lys Pro Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp Asp Thr Leu  
 145 150 155 160  
 Phe Gly Gly Phe Asn Arg Leu Asn His Thr Ala Glu Tyr Phe Thr Ser  
 165 170 175  
 Glu Gly Trp Tyr Asp Asp Arg Pro Arg Ser Phe Leu Val Tyr Ala Pro  
 180 185 190  
 Ser Arg Thr Ala Val Val Tyr Ala Leu Ala Asp Gly Val Glu Ser Glu  
 195 200 205  
 Pro Ile Glu Leu Ser  
 210

<210> 23  
 <211> 258  
 <212> PRT  
 <213> Zea mays

<400> 23  
 Pro Ala Ser Pro Thr Ile Asp Arg Gly Ile Ala Leu Gln Lys Met Ile  
 1 5 10 15  
 His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met  
 20 25 30  
 Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly  
 35 40 45  
 Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Val Asp  
 50 55 60  
 Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met  
 65 70 75 80  
 Asn Ala Leu Asp Glu Arg Phe Ser Phe Leu Ser Ser Ser Lys Gln Ile  
 85 90 95



Val Ser Asp Met Asn Asp Glu Glu Lys Val Ile Val Phe Glu Arg Gly  
 100 105 110  
 Asp Leu Val Phe Val Phe Asn Phe His Pro Lys Lys Thr Tyr Glu Gly  
 115 120 125  
 Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala Leu Asp  
 130 135 140  
 Ser Asp Ala Leu Val Phe Gly Gly His Gly Arg Val Gly His Asp Val  
 145 150 155 160  
 Asp His Phe Thr Ser Pro Glu Gly Val Pro Gly Val Pro Glu Thr Asn  
 165 170 175  
 Phe Asn Asn Arg Pro Asn Ser Phe Lys Val Leu Ser Pro Pro Arg Thr  
 180 185 190  
 Cys Val Ala Tyr Tyr Arg Val Asp Glu Ala Gly Ala Gly Arg Arg Leu  
 195 200 205  
 His Ala Lys Ala Glu Thr Gly Lys Thr Ser Pro Ala Glu Ser Ile Asp  
 210 215 220  
 Val Lys Ala Ser Arg Ala Ser Ser Lys Glu Asp Lys Glu Ala Thr Ala  
 225 230 235 240  
 Gly Gly Lys Lys Gly Trp Lys Phe Ala Arg Gln Pro Ser Asp Gln Asp  
 245 250 255  
 Thr Lys

<210> 24  
 <211> 210  
 <212> PRT  
 <213> *Oryza sativa*

<400> 24  
 Pro Ala Ser Pro Thr Ile Asn Arg Gly Ile Ala Leu Gln Lys Met Ile  
 1 5 10 15  
 His Phe Ile Thr Met Ala Leu Gly Gly Asp Gly Tyr Leu Asn Phe Met  
 20 25 30  
 Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Glu Gly  
 35 40 45  
 Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Ser Leu Val Asp  
 50 55 60  
 Thr Asp His Leu Arg Tyr Lys Tyr Met Asn Ala Phe Asp Gln Ala Met  
 65 70 75 80

Asn	Ala	Leu	Glu	Glu	Glu	Phe	Ser	Phe	Leu	Ser	Ser	Ser	Lys	Gln	Ile
				85											
Val	Ser	Asp	Met	Asn	Glu	Lys	Asp	Lys	Val	Ile	Val	Phe	Glu	Arg	Gly
				100											
Asp	Leu	Val	Phe	Val	Phe	Asn	Phe	His	Pro	Asn	Lys	Thr	Tyr	Lys	Gly
				115											
Tyr	Lys	Val	Gly	Cys	Asp	Leu	Pro	Gly	Lys	Tyr	Arg	Val	Ala	Leu	Asp
				130											
Ser	Asp	Ala	Leu	Val	Phe	Gly	Gly	His	Gly	Arg	Val	Gly	His	Asp	Val
				145											
Asp	His	Phe	Thr	Ser	Pro	Glu	Gly	Met	Pro	Gly	Val	Pro	Glu	Thr	Asn
				165											
Phe	Asn	Asn	Arg	Pro	Asn	Ser	Phe	Lys	Val	Leu	Ser	Pro	Pro	Arg	Thr
				180											
Cys	Val	Ala	Tyr	Tyr	Arg	Val	Asp	Glu	Asp	Arg	Glu	Glu	Leu	Arg	Arg
				195											
Gly	Gly														
		210													

```
<210> 25
<211> 210
<212> PRT
<213> Solanum tuberosum
```

```

<400> 25
Asp Ala Ser Pro Val Val Asp Ala Gly Ile Ala Leu Asp Lys Met Ile
1          5          10          15

His Phe Phe Thr Met Ala Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met
          20          25          30

Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Ser Glu Gly
          35          40          45

Asn Asn Trp Ser Tyr Asp Lys Cys Arg Arg Gln Trp Asn Leu Ala Asp
          50          55          60

Ser Glu His Leu Arg Tyr Lys Phe Met Asn Ala Phe Asp Arg Ala Met
65          70          75          80

Asn Ser Leu Asp Glu Lys Phe Ser Phe Leu Ala Ser Gly Lys Gln Ile
          85          90          95

```

Val Ser Ser Met Asp Asp Asp Asn Lys Val Val Val Phe Glu Arg Gly  
100 105 110

Asp Leu Val Phe Val Phe Asn Phe His Pro Asn Asn Thr Tyr Glu Gly  
115 120 125

Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala Leu Asp  
130 135 140

Ser Asp Ala Trp Glu Phe Gly Gly His Gly Arg Ala Gly His Asp Val  
145 150 155 160

Asp His Phe Thr Ser Pro Glu Gly Ile Pro Gly Val Pro Glu Thr Asn  
165 170 175

Phe Asn Gly Arg Pro Asn Ser Phe Lys Val Leu Ser Pro Ala Arg Thr  
180 185 190

Cys Val Ala Tyr Tyr Arg Val Asp Glu Arg Met Ser Glu Thr Glu Asp  
195 200 205

Tyr Gln  
210

<210> 26  
<211> 195  
<212> PRT  
<213> Homo sapiens

<400> 26  
Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile  
1 5 10 15

Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met  
20 25 30

Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly  
35 40 45

Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp  
50 55 60

Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met  
65 70 75 80

Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr  
85 90 95

Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala  
100 105 110

Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp  
115 120 125

Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp  
 130 135 140

Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr  
 145 150 155 160

Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu  
 165 170 175

Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp  
 180 185 190

Leu Pro Asn  
 195

<210> 27  
 <211> 60  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 ggctatctca atttcatggg taatgaattt gggcatcctg aatgggttaga cttcccaaga 60

<210> 28  
 <211> 60  
 <212> DNA  
 <213> Lathyrus sp.

<400> 28  
 gggatatttga attttatggg gaatgaattc ggacatcctg agtggatcga ttttccaagg 60

<210> 29  
 <211> 60  
 <212> DNA  
 <213> Solanum tuberosum

<400> 29  
 gggtagctca atttcatggg taacgagttt ggccatcctg agtggattga cttccctagt 60

<210> 30  
 <211> 60  
 <212> DNA  
 <213> Zea mays

<400> 30  
 ggctacttga attttatggg aaatgagttt ggtcacccag aatggattga ctttccaaga 60

<210> 31  
 <211> 60  
 <212> DNA  
 <213> Zea mays

<400> 31  
 ggctatcttta atttcatggg aaatgagttt ggacatcctg aatggataga tttccaaga 60

<210> 32  
 <211> 60  
 <212> DNA  
 <213> Oryza sativa

<400> 32  
 ggctacttaa attttatggg caatgagttt ggccatccag aatggattga cttccaaga 60

<210> 33  
 <211> 692  
 <212> PRT  
 <213> Solanum tuberosum

<400> 33  
 Ile Tyr Glu Ile Asp Pro Leu Leu Thr Asn Tyr Arg Gln His Leu Asp  
 1 5 10 15  
 Tyr Arg Tyr Ser Gln Tyr Lys Lys Leu Arg Glu Ala Ile Asp Lys Tyr  
 20 25 30  
 Glu Gly Gly Leu Glu Ala Phe Ser Arg Gly Tyr Glu Lys Met Gly Phe  
 35 40 45  
 Thr Arg Ser Ala Thr Gly Ile Thr Tyr Arg Glu Trp Ala Leu Gly Ala  
 50 55 60  
 Gln Ser Ala Ala Leu Ile Gly Asp Phe Asn Asn Trp Asp Ala Asn Ala  
 65 70 75 80  
 Asp Ile Met Thr Arg Asn Glu Phe Gly Val Trp Glu Ile Phe Leu Pro  
 85 90 95  
 Asn Asn Val Asp Gly Ser Pro Ala Ile Pro His Gly Ser Arg Val Lys  
 100 105 110  
 Ile Arg Met Asp Thr Pro Ser Gly Val Lys Asp Ser Ile Pro Ala Trp  
 115 120 125  
 Ile Asn Tyr Ser Leu Gln Leu Pro Asp Glu Ile Pro Tyr Asn Gly Ile  
 130 135 140  
 His Tyr Asp Pro Pro Glu Glu Arg Tyr Ile Phe Gln His Pro Arg  
 145 150 155 160

Pro	Lys	Lys	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	Ser	His	Ile	Gly	Met	165	170	175
Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Ser	Tyr	Val	Asn	Phe	Arg	Asp	Glu	180	185	190
Val	Leu	Pro	Arg	Ile	Lys	Lys	Leu	Gly	Tyr	Asn	Ala	Leu	Gln	Ile	Met	195	200	205
Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Ala	Ser	Phe	Gly	Tyr	His	Val	Thr	210	215	220
Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	Thr	Pro	Asp	Asp	Leu	Lys	225	230	235
Ser	Leu	Ile	Asp	Lys	Ala	His	Glu	Leu	Gly	Ile	Val	Val	Leu	Met	Asp	245	250	255
Ile	Val	His	Ser	His	Ala	Ser	Asn	Asn	Thr	Leu	Asp	Gly	Leu	Asn	Met	260	265	270
Phe	Asp	Cys	Thr	Asp	Ser	Cys	Tyr	Phe	His	Ser	Gly	Ala	Arg	Gly	Tyr	275	280	285
His	Trp	Met	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	Gly	Asn	Trp	Glu	Val	290	295	300
Leu	Arg	Tyr	Leu	Leu	Ser	Asn	Ala	Arg	Trp	Trp	Leu	Asp	Ala	Phe	Lys	305	310	315
Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	Ser	Met	Met	Tyr	Ile	His	325	330	335
His	Gly	Leu	Ser	Val	Gly	Phe	Thr	Gly	Asn	Tyr	Glu	Glu	Tyr	Phe	Gly	340	345	350
Leu	Ala	Thr	Asp	Val	Asp	Ala	Val	Val	Tyr	Leu	Met	Leu	Val	Asn	Asp	355	360	365
Leu	Ile	His	Gly	Leu	Phe	Pro	Asp	Ala	Ile	Thr	Ile	Gly	Glu	Asp	Val	370	375	380
Ser	Gly	Met	Pro	Thr	Phe	Cys	Ile	Pro	Val	Gln	Glu	Gly	Gly	Val	Gly	385	390	395
Phe	Asp	Tyr	Arg	Leu	His	Met	Ala	Ile	Ala	Asp	Lys	Arg	Ile	Glu	Leu	405	410	415
Leu	Lys	Lys	Arg	Asp	Glu	Asp	Trp	Arg	Val	Gly	Asp	Ile	Val	His	Thr	420	425	430
Leu	Thr	Asn	Arg	Arg	Trp	Ser	Glu	Lys	Cys	Val	Ser	Tyr	Ala	Glu	Ser	435	440	445

His Asp Gln Ala Leu Val Gly Asp Lys Thr Ile Ala Phe Trp Leu Met  
 450 455 460  
 Asp Lys Asp Met Tyr Asp Phe Met Ala Leu Asp Arg Pro Ser Thr Ser  
 465 470 475 480  
 Leu Ile Asp Arg Gly Ile Ala Leu His Lys Met Ile Arg Leu Val Thr  
 485 490 495  
 Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe  
 500 505 510  
 Gly His Pro Glu Trp Ile Asp Phe Pro Arg Ala Glu Gln His Leu Ser  
 515 520 525  
 Asp Gly Ser Val Ile Pro Gly Asn Gln Phe Ser Tyr Asp Lys Cys Arg  
 530 535 540  
 Arg Arg Phe Asp Leu Gly Asp Ala Glu Tyr Leu Arg Tyr Arg Gly Leu  
 545 550 555 560  
 Gln Glu Phe Asp Arg Pro Met Gln Tyr Leu Glu Asp Lys Tyr Glu Phe  
 565 570 575  
 Met Thr Ser Glu His Gln Phe Ile Ser Arg Lys Asp Glu Gly Asp Arg  
 580 585 590  
 Met Ile Val Phe Glu Lys Gly Asn Leu Val Phe Val Phe Asn Phe His  
 595 600 605  
 Trp Thr Lys Ser Tyr Ser Asp Tyr Arg Ile Ala Cys Leu Lys Pro Gly  
 610 615 620  
 Lys Tyr Lys Val Ala Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly Phe  
 625 630 635 640  
 Gly Arg Ile Asp His Asn Ala Glu Tyr Phe Thr Phe Glu Gly Trp Tyr  
 645 650 655  
 Asp Asp Arg Pro Arg Ser Ile Met Val Tyr Ala Pro Cys Lys Thr Ala  
 660 665 670  
 Val Val Tyr Ala Leu Val Asp Lys Glu Glu Glu Glu Glu Glu Glu  
 675 680 685  
 Glu Glu Glu Val  
 690

&lt;210&gt; 34

&lt;211&gt; 695

&lt;212&gt; PRT

&lt;213&gt; Solanum tuberosum

<400> 34  
 Leu Leu Asn Leu Asp Pro Thr Leu Glu Pro Tyr Leu Asp His Phe Arg  
 1 5 10 15  
 His Arg Met Lys Arg Tyr Val Asp Gln Lys Met Leu Ile Glu Lys Tyr  
 20 25 30  
 Glu Gly Pro Leu Glu Glu Phe Ala Gln Gly Tyr Leu Lys Phe Gly Phe  
 35 40 45  
 Asn Arg Glu Asp Gly Cys Ile Val Tyr Arg Glu Trp Ala Pro Ala Ala  
 50 55 60  
 Gln Glu Ala Glu Val Ile Gly Asp Phe Asn Gly Trp Asn Gly Ser Asn  
 65 70 75 80  
 His Met Met Glu Lys Asp Gln Phe Gly Val Trp Ser Ile Arg Ile Pro  
 85 90 95  
 Asp Val Asp Ser Lys Pro Val Ile Pro His Asn Ser Arg Val Lys Phe  
 100 105 110  
 Arg Phe Lys His Gly Asn Gly Val Trp Val Asp Arg Ile Pro Ala Trp  
 115 120 125  
 Ile Lys Tyr Ala Thr Ala Asp Ala Thr Lys Phe Ala Ala Pro Tyr Asp  
 130 135 140  
 Gly Val Tyr Trp Asp Pro Pro Pro Ser Glu Arg Tyr His Phe Lys Tyr  
 145 150 155 160  
 Pro Arg Pro Pro Lys Pro Arg Ala Pro Arg Ile Tyr Glu Ala His Val  
 165 170 175  
 Gly Met Ser Ser Ser Glu Pro Arg Val Asn Ser Tyr Arg Glu Phe Ala  
 180 185 190  
 Asp Asp Val Leu Pro Arg Ile Lys Ala Asn Asn Tyr Asn Thr Val Gln  
 195 200 205  
 Leu Met Ala Ile Met Glu His Ser Tyr Tyr Gly Ser Phe Gly Tyr His  
 210 215 220  
 Val Thr Asn Phe Phe Ala Val Ser Asn Arg Tyr Gly Asn Pro Glu Asp  
 225 230 235 240  
 Leu Lys Tyr Leu Ile Asp Lys Ala His Ser Leu Gly Leu Gln Val Leu  
 245 250 255  
 Val Asp Val Val His Ser His Ala Ser Asn Asn Val Thr Asp Gly Leu  
 260 265 270  
 Asn Gly Phe Asp Ile Gly Gln Gly Ser Gln Glu Ser Tyr Phe His Ala  
 275 280 285



Gly	Glu	Arg	Gly	Tyr	His	Lys	Leu	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	290	295	300
Ala	Asn	Trp	Glu	Val	Leu	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Arg	Trp	Trp	305	310	315
Leu	Glu	Glu	Tyr	Asn	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Ile	Thr	Ser	325	330	335
Met	Leu	Tyr	Val	His	His	Gly	Ile	Asn	Met	Gly	Phe	Thr	Gly	Asn	Tyr	340	345	350
Asn	Glu	Tyr	Phe	Ser	Glu	Ala	Thr	Asp	Val	Asp	Ala	Val	Val	Tyr	Leu	355	360	365
Met	Leu	Ala	Asn	Asn	Leu	Ile	His	Lys	Ile	Phe	Pro	Asp	Ala	Thr	Val	370	375	380
Ile	Ala	Glu	Asp	Val	Ser	Gly	Met	Pro	Gly	Leu	Ser	Arg	Pro	Val	Ser	385	390	395
Glu	Gly	Gly	Ile	Gly	Phe	Asp	Tyr	Arg	Leu	Ala	Met	Ala	Ile	Pro	Asp	405	410	415
Lys	Trp	Ile	Asp	Tyr	Leu	Lys	Asn	Lys	Asn	Asp	Glu	Asp	Trp	Ser	Met	420	425	430
Lys	Glu	Val	Thr	Ser	Ser	Leu	Thr	Asn	Arg	Arg	Tyr	Thr	Glu	Lys	Cys	435	440	445
Ile	Ala	Tyr	Ala	Glu	Ser	His	Asp	Gln	Ser	Ile	Val	Gly	Asp	Lys	Thr	450	455	460
Ile	Ala	Phe	Leu	Leu	Met	Asp	Lys	Glu	Met	Tyr	Ser	Gly	Met	Ser	Cys	465	470	475
Leu	Thr	Asp	Ala	Ser	Pro	Val	Val	Asp	Arg	Gly	Ile	Ala	Leu	His	Lys	485	490	495
Met	Ile	His	Phe	Phe	Thr	Met	Ala	Leu	Gly	Gly	Glu	Gly	Tyr	Leu	Asn	500	505	510
Phe	Met	Gly	Asn	Glu	Phe	Gly	His	Pro	Glu	Trp	Ile	Asp	Phe	Pro	Arg	515	520	525
Glu	Gly	Asn	Asn	Trp	Ser	Tyr	Asp	Lys	Cys	Arg	Arg	Gln	Trp	Asn	Leu	530	535	540
Ala	Asp	Ser	Glu	His	Leu	Arg	Tyr	Lys	Phe	Met	Asn	Ala	Phe	Asp	Arg	545	550	555
Ala	Met	Asn	Ser	Leu	Asp	Glu	Lys	Phe	Ser	Phe	Leu	Ala	Ser	Gly	Lys	565	570	575

Gln Ile Val Ser Ser Met Asp Asp Asp Asn Lys Val Val Val Phe Glu  
 580 585 590  
 Arg Gly Asp Leu Val Phe Val Phe Asn Phe His Pro Asn Asn Thr Tyr  
 595 600 605  
 Glu Gly Tyr Lys Val Gly Cys Asp Leu Pro Gly Lys Tyr Arg Val Ala  
 610 615 620  
 Leu Gly Ser Asp Ala Trp Glu Phe Gly Gly His Gly Arg Ala Gly His  
 625 630 635 640  
 Asp Val Asp His Phe Thr Ser Pro Glu Gly Ile Pro Gly Val Pro Glu  
 645 650 655  
 Thr Asn Phe Asn Gly Arg Pro Asn Ser Phe Lys Val Leu Ser Pro Ala  
 660 665 670  
 Arg Thr Cys Val Ala Tyr Tyr Arg Val Asp Glu Arg Met Ser Glu Thr  
 675 680 685  
 Glu Asp Tyr Gln Thr Asp Ile  
 690 695

<210> 35  
 <211> 873  
 <212> PRT  
 <213> Solanum tuberosum

<400> 35  
 Met Val Tyr Thr Leu Ser Gly Val Arg Phe Pro Thr Val Pro Ser Val  
 1 5 10 15  
 Tyr Lys Ser Asn Gly Phe Ser Ser Asn Gly Asp Arg Arg Asn Ala Asn  
 20 25 30  
 Val Ser Val Phe Leu Lys Lys His Ser Leu Ser Arg Lys Ile Leu Ala  
 35 40 45  
 Glu Lys Ser Ser Tyr Asn Ser Glu Phe Arg Pro Ser Thr Val Ala Ala  
 50 55 60  
 Ser Gly Lys Val Leu Val Pro Gly Thr Gln Ser Asp Ser Ser Ser Ser  
 65 70 75 80  
 Ser Thr Asp Gln Phe Glu Phe Thr Glu Thr Ser Pro Glu Asn Ser Pro  
 85 90 95  
 Ala Ser Thr Asp Val Asp Ser Ser Thr Met Glu His Ala Ser Gln Ile  
 100 105 110

Lys	Thr	Glu	Asn	Asp	Asp	Val	Glu	Pro	Ser	Ser	Asp	Leu	Thr	Gly	Ser	115	120	125	
Val	Glu	Glu	Leu	Asp	Phe	Ala	Ser	Ser	Leu	Gln	Leu	Gln	Glu	Gly	Gly	130	135	140	
Lys	Leu	Glu	Glu	Ser	Lys	Thr	Leu	Asn	Thr	Ser	Glu	Glu	Thr	Ile	Ile	145	150	155	160
Asp	Glu	Ser	Asp	Arg	Ile	Arg	Glu	Arg	Gly	Ile	Pro	Pro	Pro	Gly	Leu	165	170	175	
Gly	Gln	Lys	Ile	Tyr	Glu	Ile	Asp	Pro	Leu	Leu	Thr	Asn	Tyr	Arg	Gln	180	185	190	
His	Leu	Asp	Tyr	Arg	Tyr	Ser	Gln	Tyr	Lys	Lys	Leu	Arg	Glu	Ala	Ile	195	200	205	
Asp	Lys	Tyr	Glu	Gly	Gly	Leu	Glu	Ala	Phe	Ser	Arg	Gly	Tyr	Glu	Lys	210	215	220	
Met	Gly	Phe	Thr	Arg	Ser	Ala	Thr	Gly	Ile	Thr	Tyr	Arg	Glu	Trp	Ala	225	230	235	240
Leu	Gly	Ala	Gln	Ser	Ala	Ala	Leu	Ile	Gly	Asp	Phe	Asn	Asn	Trp	Asp	245	250	255	
Ala	Asn	Ala	Asp	Ile	Met	Thr	Arg	Asn	Glu	Phe	Gly	Val	Trp	Glu	Ile	260	265	270	
Phe	Leu	Pro	Asn	Asn	Val	Asp	Gly	Ser	Pro	Ala	Ile	Pro	His	Gly	Ser	275	280	285	
Arg	Val	Lys	Ile	Arg	Met	Asp	Thr	Pro	Ser	Gly	Val	Lys	Asp	Ser	Ile	290	295	300	
Pro	Ala	Trp	Ile	Asn	Tyr	Ser	Leu	Gln	Leu	Pro	Asp	Glu	Ile	Pro	Tyr	305	310	315	320
Asn	Gly	Ile	His	Tyr	Asp	Pro	Pro	Glu	Glu	Glu	Arg	Tyr	Ile	Phe	Gln	325	330	335	
His	Pro	Arg	Pro	Lys	Lys	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	Ser	His	340	345	350	
Ile	Gly	Met	Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Ser	Tyr	Val	Asn	Phe	355	360	365	
Arg	Asp	Glu	Val	Leu	Pro	Arg	Ile	Lys	Lys	Leu	Gly	Tyr	Asn	Ala	Leu	370	375	380	
Gln	Ile	Met	Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Ala	Ser	Phe	Gly	Tyr	385	390	395	400

His	Val	Thr	Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	Thr	Pro	Asp	
				405					410					415		
Asp	Leu	Lys	Ser	Leu	Ile	Asp	Lys	Ala	His	Glu	Leu	Gly	Ile	Val	Val	
			420					425					430			
Leu	Met	Asp	Ile	Val	His	Ser	His	Ala	Ser	Asn	Asn	Thr	Leu	Asp	Gly	
		435					440					445				
Leu	Asn	Met	Phe	Asp	Cys	Thr	Asp	Ser	Cys	Tyr	Phe	His	Ser	Gly	Ala	
	450					455					460					
Arg	Gly	Tyr	His	Trp	Met	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	Gly	Asn	
465					470					475					480	
Trp	Glu	Val	Leu	Arg	Tyr	Leu	Leu	Ser	Asn	Ala	Arg	Trp	Trp	Leu	Asp	
				485					490					495		
Ala	Phe	Lys	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	Ser	Met	Met	
			500					505					510			
Tyr	Ile	His	His	Gly	Leu	Ser	Val	Gly	Phe	Thr	Gly	Asn	Tyr	Glu	Glu	
	515						520					525				
Tyr	Phe	Gly	Leu	Ala	Thr	Asp	Val	Asp	Ala	Val	Val	Tyr	Leu	Met	Leu	
	530					535					540					
Val	Asn	Asp	Leu	Ile	His	Gly	Leu	Phe	Pro	Asp	Ala	Ile	Thr	Ile	Gly	
545					550					555					560	
Glu	Asp	Val	Ser	Gly	Met	Pro	Thr	Phe	Cys	Ile	Pro	Val	Gln	Glu	Gly	
				565					570					575		
Gly	Val	Gly	Phe	Asp	Tyr	Arg	Leu	His	Met	Ala	Ile	Ala	Asp	Lys	Arg	
			580					585					590			
Ile	Glu	Leu	Leu	Lys	Lys	Arg	Asp	Glu	Asp	Trp	Arg	Val	Gly	Asp	Ile	
	595						600						605			
Val	His	Thr	Leu	Thr	Asn	Arg	Arg	Trp	Ser	Glu	Lys	Cys	Val	Ser	Tyr	
	610					615					620					
Ala	Glu	Ser	His	Asp	Gln	Ala	Leu	Val	Gly	Asp	Lys	Thr	Ile	Ala	Phe	
625					630					635					640	
Trp	Leu	Met	Asp	Lys	Asp	Met	Tyr	Asp	Phe	Met	Ala	Leu	Asp	Arg	Pro	
				645					650					655		
Ser	Thr	Ser	Leu	Ile	Asp	Arg	Gly	Ile	Ala	Leu	His	Lys	Met	Ile	Arg	
			660					665					670			
Leu	Val	Thr	Met	Gly	Leu	Gly	Gly	Glu	Gly	Tyr	Leu	Asn	Phe	Met	Gly	
		675					680					685				

Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Ala Glu Gln  
 690 695 700  
 His Leu Ser Asp Gly Ser Val Ile Pro Gly Asn Gln Phe Ser Tyr Asp  
 705 710 715 720  
 Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Glu Tyr Leu Arg Tyr  
 725 730 735  
 Arg Gly Leu Gln Glu Phe Asp Arg Pro Met Gln Tyr Leu Glu Asp Lys  
 740 745 750  
 Tyr Glu Phe Met Thr Ser Glu His Gln Phe Ile Ser Arg Lys Asp Glu  
 755 760 765  
 Gly Asp Arg Met Ile Val Phe Glu Lys Gly Asn Leu Val Phe Val Phe  
 770 775 780  
 Asn Phe His Trp Thr Lys Ser Tyr Ser Asp Tyr Arg Ile Ala Cys Leu  
 785 790 795 800  
 Lys Pro Gly Lys Tyr Lys Val Ala Leu Asp Ser Asp Asp Pro Leu Phe  
 805 810 815  
 Gly Gly Phe Gly Arg Ile Asp His Asn Ala Glu Tyr Phe Thr Phe Glu  
 820 825 830  
 Gly Trp Tyr Asp Asp Arg Pro Arg Ser Ile Met Val Tyr Ala Pro Cys  
 835 840 845  
 Lys Thr Ala Val Val Tyr Ala Leu Val Asp Lys Glu Glu Glu Glu Glu  
 850 855 860  
 Glu Glu Glu Glu Glu Glu Val Ala Ala  
 865 870

<210> 36  
 <211> 861  
 <212> PRT  
 <213> Lathyrus sp.

<400> 36  
 Met Val Tyr Thr Ile Ser Gly Ile Arg Phe Pro Val Leu Pro Ser Leu  
 1 5 10 15  
 His Lys Ser Thr Leu Arg Cys Asp Arg Arg Ala Ser Ser His Ser Phe  
 20 25 30  
 Phe Leu Lys Asn Asn Ser Ser Ser Phe Ser Arg Thr Ser Leu Tyr Ala  
 35 40 45  
 Lys Phe Ser Arg Asp Ser Glu Thr Lys Ser Ser Thr Ile Ala Glu Ser  
 50 55 60

Asp	Lys	Val	Leu	Ile	Pro	Glu	Asp	Gln	Asp	Asn	Ser	Val	Ser	Leu	Ala	65	70	75	80
Asp	Gln	Leu	Glu	Asn	Pro	Asp	Ile	Thr	Ser	Glu	Asp	Ala	Gln	Asn	Leu	85	90	95	
Glu	Asp	Leu	Thr	Met	Lys	Asp	Gly	Asn	Lys	Tyr	Asn	Ile	Asp	Glu	Ser	100	105	110	
Thr	Ser	Ser	Tyr	Arg	Glu	Val	Gly	Asp	Glu	Lys	Gly	Ser	Val	Thr	Ser	115	120	125	
Ser	Ser	Leu	Val	Asp	Val	Asn	Thr	Asp	Thr	Gln	Ala	Lys	Lys	Thr	Ser	130	135	140	
Val	His	Ser	Asp	Lys	Lys	Val	Lys	Val	Asp	Lys	Pro	Lys	Ile	Ile	Pro	145	150	155	160
Pro	Pro	Gly	Ser	Gly	Gln	Lys	Ile	Tyr	Glu	Ile	Asp	Pro	Leu	Leu	Gln	165	170	175	
Ala	His	Arg	Gln	His	Leu	Asp	Phe	Arg	Tyr	Gly	Gln	Tyr	Lys	Arg	Ile	180	185	190	
Arg	Glu	Glu	Ile	Asp	Lys	Tyr	Glu	Gly	Gly	Leu	Asp	Ala	Phe	Ser	Arg	195	200	205	
Gly	Tyr	Glu	Lys	Phe	Gly	Phe	Thr	Arg	Ser	Ala	Thr	Gly	Ile	Thr	Tyr	210	215	220	
Arg	Glu	Trp	Gly	Pro	Gly	Ala	Lys	Ser	Ala	Ala	Leu	Val	Gly	Asp	Phe	225	230	235	240
Asn	Asn	Trp	Asn	Pro	Asn	Ala	Asp	Val	Met	Thr	Lys	Asp	Ala	Phe	Gly	245	250	255	
Val	Trp	Glu	Ile	Phe	Leu	Pro	Asn	Asn	Ala	Asp	Gly	Ser	Pro	Pro	Ile	260	265	270	
Pro	His	Gly	Ser	Arg	Val	Lys	Ile	His	Met	Asp	Thr	Pro	Ser	Gly	Ile	275	280	285	
Lys	Asp	Ser	Ile	Pro	Ala	Trp	Ile	Lys	Phe	Ser	Val	Gln	Ala	Pro	Gly	290	295	300	
Glu	Ile	Pro	Tyr	Asn	Gly	Ile	Tyr	Tyr	Asp	Pro	Pro	Glu	Glu	Glu	Lys	305	310	315	320
Tyr	Val	Phe	Lys	His	Pro	Gln	Pro	Lys	Arg	Pro	Gln	Ser	Ile	Arg	Ile	325	330	335	
Tyr	Glu	Ser	His	Ile	Gly	Met	Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Thr	340	345	350	

Tyr Ala Asn Phe Arg Asp Asp Val Leu Pro Arg Ile Lys Lys Leu Gly  
 355 360 365  
 Tyr Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala  
 370 375 380  
 Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe  
 385 390 395 400  
 Gly Thr Pro Glu Asp Leu Lys Ser Leu Ile Asp Arg Ala His Glu Leu  
 405 410 415  
 Gly Leu Leu Val Leu Met Asp Ile Val His Ser His Ser Ser Asn Asn  
 420 425 430  
 Thr Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Gly His Tyr Phe  
 435 440 445  
 His Pro Gly Ser Arg Gly Tyr His Trp Met Trp Asp Ser Arg Leu Phe  
 450 455 460  
 Asn Tyr Gly Ser Trp Glu Val Leu Arg Tyr Leu Leu Ser Asn Ala Arg  
 465 470 475 480  
 Trp Trp Leu Asp Glu Tyr Lys Phe Asp Gly Phe Arg Phe Asp Gly Val  
 485 490 495  
 Thr Ser Met Met Tyr Thr His His Gly Leu Gln Val Ser Phe Thr Gly  
 500 505 510  
 Asn Tyr Ser Glu Tyr Phe Gly Leu Ala Thr Asp Val Glu Ala Val Val  
 515 520 525  
 Tyr Met Met Leu Val Asn Asp Leu Ile His Gly Leu Phe Pro Glu Ala  
 530 535 540  
 Val Ser Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Cys Leu Pro  
 545 550 555 560  
 Thr Gln Asp Gly Gly Ile Gly Phe Asn Tyr Arg Leu His Met Ala Val  
 565 570 575  
 Ala Asp Lys Trp Ile Glu Leu Leu Lys Lys Gln Asp Glu Asp Trp Arg  
 580 585 590  
 Met Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Leu Glu Lys  
 595 600 605  
 Cys Val Val Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys  
 610 615 620  
 Thr Leu Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala  
 625 630 635 640

Leu Asp Arg Pro Ser Thr Pro Leu Ile Asp Arg Gly Ile Ala Leu His  
 645 650 655  
 Lys Met Ile Arg Leu Ile Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu  
 660 665 670  
 Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro  
 675 680 685  
 Arg Gly Glu Gln His Leu Pro Asn Gly Lys Ile Val Pro Gly Asn Asn  
 690 695 700  
 Asn Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Asp  
 705 710 715 720  
 Tyr Leu Arg Tyr His Gly Met Gln Glu Phe Asp Arg Ala Met Gln His  
 725 730 735  
 Leu Glu Glu Thr Tyr Gly Phe Met Thr Ser Glu His Gln Tyr Ile Ser  
 740 745 750  
 Arg Lys Asn Glu Gly Asp Arg Val Ile Ile Phe Glu Arg Asp Asn Leu  
 755 760 765  
 Val Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Lys  
 770 775 780  
 Val Gly Cys Leu Lys Pro Gly Lys Tyr Lys Ile Val Leu Asp Ser Asp  
 785 790 795 800  
 Asp Thr Leu Phe Gly Gly Phe Asn Arg Leu Asn His Thr Ala Glu Tyr  
 805 810 815  
 Phe Thr Ser Glu Gly Trp Tyr Asp Asp Arg Pro Arg Ser Phe Leu Val  
 820 825 830  
 Tyr Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Ala Asp Gly Val  
 835 840 845  
 Glu Ser Glu Pro Ile Glu Leu Ser Asp Gly Val Glu Ser  
 850 855 860

<210> 37  
 <211> 2531  
 <212> DNA  
 <213> Solanum tuberosum

<220>  
 <221> CDS  
 <222> (5) .. (2530)

<220>



<221> modified\_base  
 <222> (2492)..(2492)  
 <223> a, c, g, t, other or unknown

<220>  
 <221> modified\_base  
 <222> (2499)..(2499)  
 <223> a, c, g, t, other or unknown

<220>  
 <221> modified\_base  
 <222> (2516)..(2516)  
 <223> a, c, g, t, other or unknown

<220>  
 <221> modified\_base  
 <222> (2520)..(2521)  
 <223> a, c, g, t, other or unknown

<400> 37  
 ggat gct aat gtt tct gta ttc ttg aaa aag cac tct ctt tca cgg aag 49  
   Ala Asn Val Ser Val Phe Leu Lys Lys His Ser Leu Ser Arg Lys  
     1                  5                  10                  15

atc ttg gct gaa aag tct tct tac aat tcc gaa tcc cga cct tct aca 97  
 Ile Leu Ala Glu Lys Ser Ser Tyr Asn Ser Glu Ser Arg Pro Ser Thr  
                   20                  25                  30

gtt gca gca tcg ggg aaa gtc ctt gtg cct gga ayc cag agt gat agc 145  
 Val Ala Ala Ser Gly Lys Val Leu Val Pro Gly Xaa Gln Ser Asp Ser  
                   35                  40                  45

tcc tca tcc tca aca gac caa ttt gag ttc act gag aca tct cca gaa 193  
 Ser Ser Ser Ser Thr Asp Gln Phe Glu Phe Thr Glu Thr Ser Pro Glu  
                   50                  55                  60

aat tcc cca gca tca act gat gta gat agt tca aca atg gaa cac gct 241  
 Asn Ser Pro Ala Ser Thr Asp Val Asp Ser Ser Thr Met Glu His Ala  
     65                  70                  75

agc cag att aaa act gag aac gat gac gtt gag ccg tca agt gat ctt 289  
 Ser Gln Ile Lys Thr Glu Asn Asp Asp Val Glu Pro Ser Ser Asp Leu  
   80                  85                  90                  95

aca gga agt gtt gaa gag ctg gat ttt gct tca tca cta caa cta caa 337  
 Thr Gly Ser Val Glu Glu Leu Asp Phe Ala Ser Ser Leu Gln Leu Gln  
                   100                  105                  110

gaa ggt ggt aaa ctg gag gag tct aaa aca tta aat act tct gaa gag 385  
 Glu Gly Gly Lys Leu Glu Glu Ser Lys Thr Leu Asn Thr Ser Glu Glu  
                   115                  120                  125

aca att att gat gaa tct gat agg atc aga gag agg ggc atc cct cca 433  
 Thr Ile Ile Asp Glu Ser Asp Arg Ile Arg Glu Arg Gly Ile Pro Pro

130	135	140	
cct gga ctt ggt cag aag att tat gaa ata gac ccc ctt ttg aca aac Pro Gly Leu Gly Gln Lys Ile Tyr Glu Ile Asp Pro Leu Leu Thr Asn 145 150 155			481
tat cgt caa cac ctt gat tac agg tat tca cag tac aag aaa ctg agg Tyr Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr Lys Lys Leu Arg 160 165 170 175			529
gag gca att gac aag tat gag ggt ggt ttg gaa gct ttt tct cgt ggt Glu Ala Ile Asp Lys Tyr Glu Gly Gly Leu Glu Ala Phe Ser Arg Gly 180 185 190			577
tat gaa aaa atg ggt ttc act cgt agt gct aca ggt atc act tac cgt Tyr Glu Lys Met Gly Phe Thr Arg Ser Ala Thr Gly Ile Thr Tyr Arg 195 200 205			625
gag tgg gct cct ggt gcc cag tca gct gcc ctc att gga gat ttc aac Glu Trp Ala Pro Gly Ala Gln Ser Ala Ala Leu Ile Gly Asp Phe Asn 210 215 220			673
aat tgg gac gca aat gct gac att atg act cgg aat gaa ttt ggt gtc Asn Trp Asp Ala Asn Ala Asp Ile Met Thr Arg Asn Glu Phe Gly Val 225 230 235			721
tgg gag att ttt ctg cca aat aat gtg gat ggt tct cct gca att cct Trp Glu Ile Phe Leu Pro Asn Asn Val Asp Gly Ser Pro Ala Ile Pro 240 245 250 255			769
cat ggg tcc aga gtg aag ata cgy atg gac act cca tca ggt gtt aag His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro Ser Gly Val Lys 260 265 270			817
gat tcc att cct gct tgg atc aac tac tct tta cag ctt cct gat gaa Asp Ser Ile Pro Ala Trp Ile Asn Tyr Ser Leu Gln Leu Pro Asp Glu 275 280 285			865
att cca tat aat gga ata tat tat gat cca ccc gaa gag gag agg tat Ile Pro Tyr Asn Gly Ile Tyr Tyr Asp Pro Pro Glu Glu Glu Arg Tyr 290 295 300			913
rtc ttc caa cac cca cgg cca aag aaa cca aag tcg ctg aga ata tat Xaa Phe Gln His Pro Arg Pro Lys Lys Pro Lys Ser Leu Arg Ile Tyr 305 310 315			961
gaa tct cat att gga atg agt agt ccg gag cct aaa att aac tca tac Glu Ser His Ile Gly Met Ser Ser Pro Glu Pro Lys Ile Asn Ser Tyr 320 325 330 335			1009
gtg aat ttt aga gat gaa gtt ctt cct cgc ata aaa aas ctt ggg tac Val Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys Xaa Leu Gly Tyr 340 345 350			1057

aat gcg gtg caa att atg gct att caa gag cat tct tat tat gct agt	1105
Asn Ala Val Gln Ile Met Ala Ile Gln Glu His Ser Tyr Tyr Ala Ser	
355 360 365	
ttt ggt tat cat gtc aca aat ttt ttt gca cca agc agc cgt ttt gga	1153
Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser Ser Arg Phe Gly	
370 375 380	
acg ccc gac gac ctt aag tct ttg att gat aaa gct cat gag cta gga	1201
Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala His Glu Leu Gly	
385 390 395	
att gtt gtt ctc atg gac att gtt cac agc cat gca tca aat aat act	1249
Ile Val Val Leu Met Asp Ile Val His Ser His Ala Ser Asn Asn Thr	
400 405 410 415	
tta gat gga ctg aac atg ttt gac ggc aca gat agt tgt tac ttt cac	1297
Leu Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His	
420 425 430	
tct gga gct cgt ggt tat cat tgg atg tgg gat tcc cgc ctc ttt aac	1345
Ser Gly Ala Arg Gly Tyr His Trp Met Trp Asp Ser Arg Leu Phe Asn	
435 440 445	
tat gga aac tgg gag gta ctt agg tat ctt ctc tca aat gcg aga tgg	1393
Tyr Gly Asn Trp Glu Val Leu Arg Tyr Leu Leu Ser Asn Ala Arg Trp	
450 455 460	
tgg ttg gat gag ttc aaa ttt gat gga ttt aga ttt gat ggt gtg aca	1441
Trp Leu Asp Glu Phe Lys Phe Asp Gly Phe Arg Phe Asp Gly Val Thr	
465 470 475	
tca atg atg tat act cac cac gga tta tcg gtg gga ttc act ggg aac	1489
Ser Met Met Tyr Thr His His Gly Leu Ser Val Gly Phe Thr Gly Asn	
480 485 490 495	
tac gag gaa tac ttt gga ctc gca act gat gtg gat gct gtt gtg tat	1537
Tyr Glu Glu Tyr Phe Gly Leu Ala Thr Asp Val Asp Ala Val Val Tyr	
500 505 510	
ctg atg ctg gtc aac gat ctt att cac ggg ctt ttc cca gat gca att	1585
Leu Met Leu Val Asn Asp Leu Ile His Gly Leu Phe Pro Asp Ala Ile	
515 520 525	
acc att ggt gaa gat gtt agc gga atg ccg aca ttt tgt att ccc gtt	1633
Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe Cys Ile Pro Val	
530 535 540	
caa gat ggg ggt gtt ggc ttt gac tat cgg ctg cat atg gca att gct	1681
Gln Asp Gly Gly Val Gly Phe Asp Tyr Arg Leu His Met Ala Ile Ala	
545 550 555	
gat aaa tgg att gag ttg ctc aag aaa cgg gat gag gat tgg aga gtg	1729
Asp Lys Trp Ile Glu Leu Leu Lys Lys Arg Asp Glu Asp Trp Arg Val	

560	565	570	575	
ggt gat att gtt cat aca ctg aca aat aga aga tgg tcg gaa aag tgt				1777
Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp Ser Glu Lys Cys	580	585	590	
gtt tca tmc gct gaa agt cat gat caa gct cta gtc ggt gat aaa act				1825
Val Ser Xaa Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys Thr	595	600	605	
ata gca tyc tgg ctg atg gac aag gat atg tat gat ttt atg gct ctg				1873
Ile Ala Xaa Trp Leu Met Asp Lys Asp Met Tyr Asp Phe Met Ala Leu	610	615	620	
gat aga ccg tca aca tca tta ata gat cgt ggg ata gca ttg cac aag				1921
Asp Arg Pro Ser Thr Ser Leu Ile Asp Arg Gly Ile Ala Leu His Lys	625	630	635	
atg att agg ctt gta act atg gga tta gga gga gaa ggg tac cta aat				1969
Met Ile Arg Leu Val Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn	640	645	650	655
ttc atg gga aat gaa ttc ggc cac cct gag tgg att gat ttc cct agg				2017
Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg	660	665	670	
gct gar caa cac ctc tct gat ggc tca gta att ccc gga aac caa ttc				2065
Ala Glu Gln His Leu Ser Asp Gly Ser Val Ile Pro Gly Asn Gln Phe	675	680	685	
agt tat gat aaa tgc aga cgg aga ttt gac ctg gga gat gca gaa tat				2113
Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly Asp Ala Glu Tyr	690	695	700	
tta aga tac cat ggg ttg caa gaa ttt gac cgg gct atg cag tat ctt				2161
Leu Arg Tyr His Gly Leu Gln Glu Phe Asp Arg Ala Met Gln Tyr Leu	705	710	715	
gaa gat aaa tat gag ttt atg act tca gaa cac cag ttc ata tca cga				2209
Glu Asp Lys Tyr Glu Phe Met Thr Ser Glu His Gln Phe Ile Ser Arg	720	725	730	735
aag gat gaa gga gat agg atg att gta ttt gaa ara gga aac cta gtt				2257
Lys Asp Glu Gly Asp Arg Met Ile Val Phe Glu Xaa Gly Asn Leu Val	740	745	750	
ttt gtc ttt aat ttt cac tgg aca aat agc tat tca gac tat cgc ata				2305
Phe Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg Ile	755	760	765	
ggc tgc ctg aag cct gga aaa tac aag gtt ggc ttg gac tca gat gat				2353
Gly Cys Leu Lys Pro Gly Lys Tyr Lys Val Gly Leu Asp Ser Asp Asp	770	775	780	

cca ctt ttt ggt ggc ttc ggg aga att gat cat aat gcc gaa tat ttc	2401
Pro Leu Phe Gly Gly Phe Gly Arg Ile Asp His Asn Ala Glu Tyr Phe	
785 790 795	
acc tct gaa gga tcg tat gat gat cgy ccy cgy yca att atg gtg tat	2449
Thr Ser Glu Gly Ser Tyr Asp Asp Arg Pro Arg Xaa Ile Met Val Tyr	
800 805 810 815	
gca cct agt aga aca gca gtg gtc tat gca cta gta gac aaa nta gaa	2497
Ala Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Asp Lys Xaa Glu	
820 825 830	
gna gaa gaa gaa gaa gaa ncc gnn gaa gaa ttt t	2531
Xaa Glu Glu Glu Glu Glu Xaa Xaa Glu Glu Phe	
835 840	

<210> 38  
 <211> 842  
 <212> PRT  
 <213> Solanum tuberosum

<220>  
 <221> MOD\_RES  
 <222> (43)..(43)  
 <223> Thr or Ile

<220>  
 <221> MOD\_RES  
 <222> (304)..(304)  
 <223> Val or Ile

<220>  
 <221> MOD\_RES  
 <222> (348)..(348)  
 <223> Lys or Asn

<220>  
 <221> MOD\_RES  
 <222> (594)..(594)  
 <223> Tyr or Ser

<220>  
 <221> MOD\_RES  
 <222> (610)..(610)  
 <223> Ser or Phe

<220>  
 <221> MOD\_RES  
 <222> (747)..(747)  
 <223> Arg or Lys

<220>  
 <221> MOD\_RES

<222> (811)..(811)

<223> Pro or Ser

<220>

<221> MOD\_RES

<222> (830)..(830)

<223> Ile, Val, or Leu

<220>

<221> MOD\_RES

<222> (832)..(832)

<223> Glu, Gly, Ala or Val

<220>

<221> MOD\_RES

<222> (838)..(838)

<223> Thr, Ala, Pro or Ser

<220>

<221> MOD\_RES

<222> (839)..(839)

<223> Glu, Asp, Gly, Ala or Val

<400> 38

Ala	Asn	Val	Ser	Val	Phe	Leu	Lys	Lys	His	Ser	Leu	Ser	Arg	Lys	Ile
1				5					10					15	

Leu	Ala	Glu	Lys	Ser	Ser	Tyr	Asn	Ser	Glu	Ser	Arg	Pro	Ser	Thr	Val
			20					25					30		

Ala	Ala	Ser	Gly	Lys	Val	Leu	Val	Pro	Gly	Xaa	Gln	Ser	Asp	Ser	Ser
		35					40					45			

Ser	Ser	Ser	Thr	Asp	Gln	Phe	Glu	Phe	Thr	Glu	Thr	Ser	Pro	Glu	Asn
	50					55					60				

Ser	Pro	Ala	Ser	Thr	Asp	Val	Asp	Ser	Ser	Thr	Met	Glu	His	Ala	Ser
65					70					75					80

Gln	Ile	Lys	Thr	Glu	Asn	Asp	Asp	Val	Glu	Pro	Ser	Ser	Asp	Leu	Thr
				85					90					95	

Gly	Ser	Val	Glu	Leu	Asp	Phe	Ala	Ser	Ser	Leu	Gln	Leu	Gln	Glu	
			100				105					110			

Gly	Gly	Lys	Leu	Glu	Glu	Ser	Lys	Thr	Leu	Asn	Thr	Ser	Glu	Glu	Thr
		115					120					125			

Ile	Ile	Asp	Glu	Ser	Asp	Arg	Ile	Arg	Glu	Arg	Gly	Ile	Pro	Pro	Pro
	130					135					140				

Gly	Leu	Gly	Gln	Lys	Ile	Tyr	Glu	Ile	Asp	Pro	Leu	Leu	Thr	Asn	Tyr
145					150					155					160

Arg	Gln	His	Leu	Asp	Tyr	Arg	Tyr	Ser	Gln	Tyr	Lys	Lys	Leu	Arg	Glu	165	170	175
Ala	Ile	Asp	Lys	Tyr	Glu	Gly	Gly	Leu	Glu	Ala	Phe	Ser	Arg	Gly	Tyr	180	185	190
Glu	Lys	Met	Gly	Phe	Thr	Arg	Ser	Ala	Thr	Gly	Ile	Thr	Tyr	Arg	Glu	195	200	205
Trp	Ala	Pro	Gly	Ala	Gln	Ser	Ala	Ala	Leu	Ile	Gly	Asp	Phe	Asn	Asn	210	215	220
Trp	Asp	Ala	Asn	Ala	Asp	Ile	Met	Thr	Arg	Asn	Glu	Phe	Gly	Val	Trp	225	230	235
Glu	Ile	Phe	Leu	Pro	Asn	Asn	Val	Asp	Gly	Ser	Pro	Ala	Ile	Pro	His	245	250	255
Gly	Ser	Arg	Val	Lys	Ile	Arg	Met	Asp	Thr	Pro	Ser	Gly	Val	Lys	Asp	260	265	270
Ser	Ile	Pro	Ala	Trp	Ile	Asn	Tyr	Ser	Leu	Gln	Leu	Pro	Asp	Glu	Ile	275	280	285
Pro	Tyr	Asn	Gly	Ile	Tyr	Tyr	Asp	Pro	Pro	Glu	Glu	Glu	Arg	Tyr	Xaa	290	295	300
Phe	Gln	His	Pro	Arg	Pro	Lys	Lys	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	305	310	315
Ser	His	Ile	Gly	Met	Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Ser	Tyr	Val	325	330	335
Asn	Phe	Arg	Asp	Glu	Val	Leu	Pro	Arg	Ile	Lys	Xaa	Leu	Gly	Tyr	Asn	340	345	350
Ala	Val	Gln	Ile	Met	Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Ala	Ser	Phe	355	360	365
Gly	Tyr	His	Val	Thr	Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	Thr	370	375	380
Pro	Asp	Asp	Leu	Lys	Ser	Leu	Ile	Asp	Lys	Ala	His	Glu	Leu	Gly	Ile	385	390	395
Val	Val	Leu	Met	Asp	Ile	Val	His	Ser	His	Ala	Ser	Asn	Asn	Thr	Leu	405	410	415
Asp	Gly	Leu	Asn	Met	Phe	Asp	Gly	Thr	Asp	Ser	Cys	Tyr	Phe	His	Ser	420	425	430
Gly	Ala	Arg	Gly	Tyr	His	Trp	Met	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	435	440	445

Gly	Asn	Trp	Glu	Val	Leu	Arg	Tyr	Leu	Leu	Ser	Asn	Ala	Arg	Trp	Trp	450	455	460	
Leu	Asp	Glu	Phe	Lys	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	Ser	465	470	475	480
Met	Met	Tyr	Thr	His	His	Gly	Leu	Ser	Val	Gly	Phe	Thr	Gly	Asn	Tyr	485	490	495	
Glu	Glu	Tyr	Phe	Gly	Leu	Ala	Thr	Asp	Val	Asp	Ala	Val	Val	Tyr	Leu	500	505	510	
Met	Leu	Val	Asn	Asp	Leu	Ile	His	Gly	Leu	Phe	Pro	Asp	Ala	Ile	Thr	515	520	525	
Ile	Gly	Glu	Asp	Val	Ser	Gly	Met	Pro	Thr	Phe	Cys	Ile	Pro	Val	Gln	530	535	540	
Asp	Gly	Gly	Val	Gly	Phe	Asp	Tyr	Arg	Leu	His	Met	Ala	Ile	Ala	Asp	545	550	555	560
Lys	Trp	Ile	Glu	Leu	Leu	Lys	Lys	Arg	Asp	Glu	Asp	Trp	Arg	Val	Gly	565	570	575	
Asp	Ile	Val	His	Thr	Leu	Thr	Asn	Arg	Arg	Trp	Ser	Glu	Lys	Cys	Val	580	585	590	
Ser	Xaa	Ala	Glu	Ser	His	Asp	Gln	Ala	Leu	Val	Gly	Asp	Lys	Thr	Ile	595	600	605	
Ala	Xaa	Trp	Leu	Met	Asp	Lys	Asp	Met	Tyr	Asp	Phe	Met	Ala	Leu	Asp	610	615	620	
Arg	Pro	Ser	Thr	Ser	Leu	Ile	Asp	Arg	Gly	Ile	Ala	Leu	His	Lys	Met	625	630	635	640
Ile	Arg	Leu	Val	Thr	Met	Gly	Leu	Gly	Gly	Glu	Gly	Tyr	Leu	Asn	Phe	645	650	655	
Met	Gly	Asn	Glu	Phe	Gly	His	Pro	Glu	Trp	Ile	Asp	Phe	Pro	Arg	Ala	660	665	670	
Glu	Gln	His	Leu	Ser	Asp	Gly	Ser	Val	Ile	Pro	Gly	Asn	Gln	Phe	Ser	675	680	685	
Tyr	Asp	Lys	Cys	Arg	Arg	Arg	Phe	Asp	Leu	Gly	Asp	Ala	Glu	Tyr	Leu	690	695	700	
Arg	Tyr	His	Gly	Leu	Gln	Glu	Phe	Asp	Arg	Ala	Met	Gln	Tyr	Leu	Glu	705	710	715	720
Asp	Lys	Tyr	Glu	Phe	Met	Thr	Ser	Glu	His	Gln	Phe	Ile	Ser	Arg	Lys	725	730	735	



Asp Glu Gly Asp Arg Met Ile Val Phe Glu Xaa Gly Asn Leu Val Phe  
 740 745 750  
 Val Phe Asn Phe His Trp Thr Asn Ser Tyr Ser Asp Tyr Arg Ile Gly  
 755 760 765  
 Cys Leu Lys Pro Gly Lys Tyr Lys Val Gly Leu Asp Ser Asp Asp Pro  
 770 775 780  
 Leu Phe Gly Gly Phe Gly Arg Ile Asp His Asn Ala Glu Tyr Phe Thr  
 785 790 795 800  
 Ser Glu Gly Ser Tyr Asp Asp Arg Pro Arg Xaa Ile Met Val Tyr Ala  
 805 810 815  
 Pro Ser Arg Thr Ala Val Val Tyr Ala Leu Val Asp Lys Xaa Glu Xaa  
 820 825 830  
 Glu Glu Glu Glu Glu Xaa Xaa Glu Glu Phe  
 835 840

<210> 39  
 <211> 3003  
 <212> DNA  
 <213> Solanum tuberosum

<400> 39  
 gatggggcct tgaactcagc aatttgacac tcagttagtt acactgccat cacttatcag 60  
 atctctatctt tttctcttaa ttccaaccaa ggaatgaata aaaagataga tttgtaaaaa 120  
 ccctaaggag agaagaagaa agatggtgta tacactctct ggagttcggt ttcctactgt 180  
 tccatcagtg tacaaatcta atggattcag cagtaatggt gatcggagga atgctaatat 240  
 ttctgtattc ttgaaaaaac actctctttc acggaagatc ttggctgaaa agtcttctta 300  
 caattccgaa tcccgacctt ctacaattgc agcatcgggg aaagtccttg tgcttggaa 360  
 ccagagtgat agctcctcat cctcaacaga tcaatttgag ttcgctgaga catctccaga 420  
 aaattcccca gcatcaactg atgtagatag ttcaacaatg gaacacgcta gccagattaa 480  
 aactgagaac gatgacgttg agccgtcaag tgatcttaca ggaagtgttg aagagctgga 540  
 ttttgcttca tcaactacaac tacaagaagg tggtaaactg gaggagtcta aaacattaaa 600  
 tactttctgaa gagacaatta ttgatgaatc tgataggatc agagagaggg gcatccctcc 660  
 acctggactt ggtcagaaga tttatgaaat agacccctt ttgacaaact atcgtcaaca 720  
 ccttgattac aggtattcac agtacaagaa actgaggagg gcaattgaca agtatgaggg 780  
 tgggttgga gctttttctc gtggttatga aagaatgggt ttcactcgta gtgctacagg 840  
 tatcacttac cgtgagtggg ctcttggtgc ccagtcagct gccctcattg gggatttcaa 900  
 caattgggac gcaaatgctg actttatgac tcggaatgaa tttggtgtct gagagatttt 960  
 tctgccaaat aatgtggatg gttctcctgc aattcctcat ggggtccagag tgaagatacg 1020  
 tatggacact ccatcaggtg ttaaggattc cattcctgct tggatcaact actctttaca 1080  
 gcttctgat gaaattccat ataattggaat atattatgat ccacccgaag aggagaggta 1140  
 tatcttccaa caccacggc caaagaaacc aaagtcggtg agaatatatg aatctcatat 1200  
 tggaatgagt agtccggagc ctaaaattaa ctcatcgtg aatttttagag atgaagtctt 1260  
 tcctcgcata aaaaaagctt gggtaaatg cgggtgcaaat tatggctatt caagagcatt 1320  
 cttattatgc tagttttggt tatcatgtca caaatttttt tgcaccaagc agccgttttg 1380  
 gaacgcccga cgaccttaag tctttgattg ataaagctca tgagctagga attgttgttc 1440  
 tcatggacat tgttcacagc catgcatcaa ataatacttt agatggactg aacatgtttg 1500  
 acggcacaga tagttgttac tttcactctg gagctcgtgg ttatcattgg atgtgggatt 1560

tccgcctctt	taactatgga	aactgggagg	tacttaggta	tcttctctca	aatgcgagat	1620
ggtggttggg	tgagttcaaa	tttgatggat	ttagatttga	tggtgtgaca	tcaatgatgt	1680
gtactcacca	cggattatcg	gtgggattca	ctgggaacta	cgaggaatac	tttggactcg	1740
caactgatgt	ggatgctgtt	gtgtatctga	tgctggtcaa	cgatcttatt	catgggcttt	1800
tcccagatgc	aattaccatt	ggtgaagatg	ttagcggaat	gccgacattt	tgtgttcccg	1860
ttcaagatgg	gggtgttggc	tttgactatc	ggctgcatat	ggcaattgct	gataaatgga	1920
ttgagttgct	caagaaacgg	gatgaggatt	ggagagtggg	tgatattggt	catacactga	1980
caaatagaag	atggtcggaa	aagtgtgttt	catacgtctga	aagtcatgat	caagctctag	2040
tcggtgataa	aactatagca	ttctggctga	tggacaagga	tatgtatgat	tttatggctc	2100
tggtagacc	gtcaacatca	ttaatagatc	gtgggtagc	attacacaag	atgattaggc	2160
ttgtaactat	gggattagga	ggagaagggg	acctaaattt	catgggaaat	gaattcggcc	2220
accctgagtg	gattgatttc	cctagggctg	aacaacacct	ctctgatggc	tcagtaattc	2280
ccagaaacca	attcagttat	gataaatgca	gacggagatt	tgacctggga	gatgcagaat	2340
atttaagata	ccgtgggttg	caagaatttg	accgggctat	gcagtatctt	gaagataaat	2400
atgagtttat	gacttcagaa	caccagttca	tatcacgaaa	ggatgaagga	gataggatga	2460
ttgtatttga	aaaaggaaac	ctagtttttg	tctttaattt	tcactggaca	aaaggctatt	2520
cagactatcg	cataggctgc	ctgaagcctg	gaaaatacaa	ggttgccctg	gactcagatg	2580
atccactttt	tggtggcttc	gggagaattg	atcataatgc	cgaatatttc	accttgaag	2640
gatggtatga	tgatcgtcct	cgttcaatta	tgggtgatgc	acctagtaga	acagcagtg	2700
tctatgcact	agtagacaaa	gaagaagaag	aagaagaaga	agtagcagta	gtagaagaag	2760
tagtagtaga	agaagaatga	acgaacttgt	gatcgcgttg	aaagatttga	acgccacata	2820
gagcttcttg	acgtatctgg	caatattgca	ttagtcttgg	cggaaatttca	tgtgacaaca	2880
ggtttgcaat	tctttccact	attagtagtg	caacgatata	cgcagagatg	aagtgtgaa	2940
caaaaacata	tgtaaaatcg	atgaatttat	gtcgaatgct	gggacgatcg	aattcctgca	3000
gcc						3003

&lt;210&gt; 40

&lt;211&gt; 2975

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

&lt;400&gt; 40

ttgatggggc	ttgaactcag	caatttgaca	ctcagttagt	tacactccta	tcacttatca	60
gatctctatt	ttttctctta	attccaacca	ggggaatgaa	taaaaggata	gatttgtaaa	120
aaccctaagg	agagaagaag	aaagatgggtg	tatatactct	ctggagttcg	ttttcctact	180
gttccatcag	tgtacaaaac	taatggattc	agcagtaatg	gtgatcggag	gaatgctaata	240
gtttctgtat	tcttgaaaaa	gcactctctt	tcacggaaga	tcttggctga	aaagtcttct	300
tacaattccg	aattccgacc	ttctacagtt	gcagcatcgg	ggaaagtcct	tgtgcctgga	360
accagagtg	atagctcctc	atcctcaaca	gaccaatttg	agttcactga	gacatctcca	420
gaaaattccc	cagcatcaac	tgatgtagat	agttcaacaa	tggaacacgc	tagccagatt	480
aaaactgaga	acgatgacgt	tgagccgtca	agtgatctta	caggaaagtgt	tgaagagctg	540
gattttgctt	catcactaca	actacaagaa	ggtggtaaac	tggaggagtc	taaaacatta	600
aatacttctg	aagagacaat	tattgatgaa	tctgatagga	tcagagagag	gggcatccct	660
ccacctggac	ttggtcagaa	gatttatgaa	atagaccccc	ttttgacaaa	ctatcgtcaa	720
caccttgatt	acaggtattc	acagtacaag	aaactgaggg	aggcaattga	caagtatgag	780
ggtgggttgg	aagcttttct	cgtgggttatg	aaaaaatggg	tttcaactcgt	agtgtacag	840
gtatcactta	ccgtgagtg	gctcctgggtg	cccagtcagc	tgccctcatt	ggagatttca	900
acaattggga	cgcaaagtct	gacattatga	ctcggaatga	atttggtgtc	tgggagattt	960
ttctgccaaa	taatgtggat	ggttctcctg	caattcctca	tgggtccaga	gtgaagatac	1020
gtatggacac	tccatcaggt	gttaaggatt	ccattcctgc	ttggatcaac	tactctttac	1080
agcttcctga	tgaatttcca	tataatggaa	tatattatga	tccacccgaa	gaggagaggt	1140
atatcttcca	acacccacgg	caaagaaac	caaagtcgct	gagaatatat	gaatctcata	1200
ttggaatgag	tagtccggag	cctaaaatta	actcatacgt	gaattttaga	gatgaagttc	1260

ttcctcgc	aaaaaagc	gggtacaat	cgctgcga	tatggctatt	caagagcatt	1320
cttattat	tagttttgg	tatcatgt	caaattttt	tgcaccaag	agccgtttt	1380
gaacgccc	cgacctta	tcttcgatt	ataaagct	tgagctag	attgttggt	1440
tcatggac	cgttcacag	catgcatca	ataatact	agatggact	aacatgttt	1500
acggcacc	tagttgttac	tttcaact	gagctcgt	ttatcatt	atgtgggatt	1560
ccgcctct	aactatgg	actgggagg	acttaggt	cttctctca	atgcgagat	1620
gtggttgg	gagttcaa	ttgatggat	tagattcg	ggtgtgac	caatgatgt	1680
tactcacc	ggattatcg	tgggattca	tgggaact	gaggaata	ttggactcg	1740
aactgatg	gatgctgt	tgtatctga	gctggcca	gatcttatt	ataggcttt	1800
cccagatg	attaccatt	gtgaagat	tgcggaat	ccgacatt	gtattcccg	1860
tcaagatg	ggtgttgg	ttgactat	gctgcata	gcaattgct	ataaatgg	1920
tgagttgc	aagaaacgg	atgaggatt	gagagtgg	gatattgtt	atacactga	1980
aaataga	tggtcggaa	agtgtgttt	atacgtga	agtcatgat	aagctctag	2040
cggtgata	actatagca	tctggctga	ggacaagg	atgtatgat	ttatggctc	2100
ggatagacc	ccaacatca	taatagat	tgggatag	ttgcacaag	tgattaggc	2160
tgtaactat	ggattagg	gagaagggt	cctaaatt	atgggaaat	aattcggcc	2220
ccctgagt	attgatttc	ctagggct	gccacacct	tctgatgg	cagtaattc	2280
cggaaacca	ttcagttat	ataaatgca	acggagatt	gacctggg	atgcagaat	2340
tttaagata	catgggttac	aagaatttg	ctgggctat	cagtatctt	aagataaata	2400
tgagtttat	acttcaga	accagttcat	atcacgaa	gatgaagg	ataggatga	2460
tgtatttg	agaggaaac	tagttttcgt	ctttaatt	cactggaca	atagctatt	2520
agactatcg	ataggctgc	tgaagcctg	aaaataca	gttgtcttg	actcagatg	2580
tccactttt	ggtggcttc	ggagaattg	tcataatgc	gaatatttc	cctctgaag	2640
atcgatgat	gatcgctct	gttcaattat	ggtgtatga	cctagtaga	cagcagtggt	2700
ctatgcact	gtagacaa	tagaagtag	agtagtaga	gaaccattg	agaatgaac	2760
gaacttgtg	tcgcgttg	agatttga	gttacttgg	catccacata	gagcttctt	2820
acatcagtc	tggcggaat	gcatgtgac	acaagggtt	cagttcttt	cactattagt	2880
agtccaccg	tatacgaga	gatgaagtgc	tgaacaaac	tatgtaaaa	cgatgaattt	2940
atgtcgaat	ctgggacgat	cgaattcctg	cagcc			2975

<210> 41  
 <211> 3033  
 <212> DNA  
 <213> Solanum tuberosum

<400> 41						
ttgatgggg	cttgaactca	gcaatttgac	actcagttag	ttacactcct	atcacttata	60
agatctctat	tttttctctt	aattccaacc	aaggaatgaa	taaaaggata	gatttgtaaa	120
aaccctaagg	agagaagaag	aaagatgggt	tatacactct	ctggagttcg	ttttcctact	180
gttccatcag	tgtacaaatc	taatggattc	agcagtaatg	gtgatcggag	gaatgctaata	240
gtttctgtat	tcttgaaaaa	gcactctctt	tcacggaaga	tcttggctga	aaagtcttct	300
tacaattccg	aattccgacc	ttctacagtt	gcagcatcgg	ggaaaagtcct	tgtgcctgga	360
accagagtg	atagctcctc	atcctcaaca	gaccaatttg	agttcactga	gacatctcca	420
gaaaattccc	cagcatcaac	tgatgtagat	agttcaaca	tggaacacgc	tagccagatt	480
aaaactgaga	acgatgacgt	tgagccgtca	agtgatctta	caggaaagtgt	tgaagagctg	540
gattttgctt	catcactaca	actacaagaa	ggtggtaaac	tggaggagtc	taaaacatta	600
aatacttctg	aagagacaat	tattgatgaa	tctgatagga	tcagagagag	gggcatccct	660
ccacctggac	ttggtcagaa	gatttatgaa	atagaccccc	ttttgacaaa	ctatcgtcaa	720
caccttgatt	acaggtattc	acagtacaag	aaactgaggg	aggcaattga	caagtatgag	780
ggtggtttgg	aagccttttc	tcgtggttat	gaaaaaatgg	gtttcactcg	tagtgctaca	840
ggtatcactt	accgtgagtg	ggctcttggg	gcccagtcag	ctgccctcat	tggagatttc	900
aacaattggg	acgcaaatgc	tgacattatg	actcggaatg	aatttggtgt	ctgggagatt	960
tttctgccaa	ataatgtgga	tggttctcct	gcaattcctc	atgggtccag	agtgaagata	1020

```

cgtatggaca ctccatcagg tgtaaggat tccattcctg cttggatcaa ctactcttta 1080
cagcttcctg atgaaattcc atataatgga atacattatg atccaccgga agaggagagg 1140
tatatcttcc aacacccacg gccaaagaaa ccaaagtcgc tgagaatata tgaatctcat 1200
attggaatga gtagtccgga gcctaaaatt aactcatacg tgaatttttag agatgaagtt 1260
cttcctcgca taaaaaagct tgggtacaat gcgctgcaaa ttatggctat tcaagagcat 1320
tcttattacg ctagtttttg ttatcatgtc acaaattttt ttgcaccaag cagccgtttt 1380
ggaacgcccc acgaccttaa gtctttgatt gataaagctc atgagctagg aattgttggt 1440
ctcatggaca ttgttcacag ccatgcatca aataatactt tagatggact gaacatgttt 1500
gactgcaccg atagttgtta ctttcactct ggagctcgtg gttatcattg gatgtgggat 1560
tcccgcctct ttaactatgg aaactgggag gtacttaggt atcttctctc aaatgcgaga 1620
tgggtggttg atgcgttcaa atttgatgga tttagatttg atggtgtgac atcaatgatg 1680
tatattcacc acggattatc ggtgggattc actgggaact acgaggaata ctttggactc 1740
gcaactgatg tggatgctgt tgtgtatctg atgctggtca acgatcttat tcatgggctt 1800
tccccagatg caattacatc tggatgaagat gttagcggaa tgccgacatt ttgtattccc 1860
gtccaagagg ggggtgttgg ctttgactat cggctgcata tggcaattgc tgataaacgg 1920
attgagttgc tcaagaaacg ggatgaggat tggagagtgg gtgatattgt tcatacactg 1980
acaaatagaa gatggtcggg aaagtgtgtt tcatacgtg aaagtcatga tcaagctcta 2040
gtcggtgata aaactatagc attctggctg atggacaagg atatgtatga ttttatggct 2100
ctggatagac cgtcaacatc attaatagat cgtgggtagg cattgcacaa gatgattagg 2160
cttgtaacta tgggattagg aggagaaggg tacctaaatt tcatgggaaa tgaattcggc 2220
caccctgagt ggattgattt ccttagggct gaacaacacc tctctgatgg ctcatgaatc 2280
cccggaaacc aattcagtta tgataaatgc agacggagat ttgacctggg agatgcagaa 2340
tatttaagat accgtgggtt gcaagaattt gaccggccta tgcagtatct tgaagataaa 2400
tatgagttta tgacttcaga acaccagttc atatcacgaa aggatgaagg agataggatg 2460
attgtatttg aaaaaggaaa cctagttttt gtctttaatt ttcactggac aaaaagctat 2520
tcagactatc gcatagcctg cctgaagcct ggaaaataca aggttgacct ggactcagat 2580
gatccacttt ttggtggctt cgggagaatt gatcataatg ccgaatatat cacttttgaa 2640
ggatggtatg atgatcgctc tcgttcaatt atggtgtatg caccttgtaa aacagcagtg 2700
gtctatgcac tagtagacaa agaagaagaa gaagaagaag aagaagaaga agaagtagca 2760
gcagtagaag aagtagtagt agaagaagaa tgaacgaact tgtgatcgcg ttgaaagatt 2820
tgaacgctac atagagcttc ttgacgtatc tggcaatatt gcatcagtct tggcgggaatt 2880
tcatgtgaca caaggtttgc aattctttcc actattagta gtgcaacgat atacgcagag 2940
atgaagtgct gaacaaacat atgtaaaatc gatgaattta tgtcgaatgc tgggacgatc 3000
gaattcctgc aggccggggg accccttagt tct 3033

```

<210> 42

<211> 847

<212> PRT

<213> Solanum tuberosum

<400> 42

Met Arg Gly Ser His His His His His His Gly Ile Leu Ala Glu Lys  
1 5 10 15

Ser Ser Tyr Asn Ser Glu Phe Arg Pro Ser Thr Val Ala Ala Ser Gly  
20 25 30

Lys Val Leu Val Pro Gly Thr Gln Ser Asp Ser Ser Ser Ser Ser Thr  
35 40 45

Asn Gln Phe Glu Phe Thr Glu Thr Ser Pro Glu Asn Ser Pro Ala Ser  
50 55 60

Thr	Asp	Val	Asp	Ser	Ser	Thr	Met	Glu	His	Ala	Ser	Gln	Ile	Lys	Thr	65	70	75	80
Glu	Asn	Asp	Asp	Val	Glu	Pro	Ser	Ser	Asp	Leu	Thr	Gly	Ser	Val	Glu	85	90	95	
Glu	Leu	Asp	Phe	Ala	Ser	Ser	Leu	Gln	Leu	Gln	Glu	Gly	Gly	Lys	Leu	100	105	110	
Glu	Glu	Ser	Lys	Thr	Leu	Asn	Thr	Ser	Glu	Glu	Thr	Ile	Ile	Asp	Glu	115	120	125	
Ser	Asp	Arg	Ile	Arg	Glu	Arg	Gly	Ile	Pro	Pro	Pro	Gly	Leu	Gly	Gln	130	135	140	
Lys	Ile	Tyr	Glu	Ile	Asp	Pro	Leu	Leu	Thr	Asn	Tyr	Arg	Gln	His	Leu	145	150	155	160
Asp	Tyr	Arg	Tyr	Ser	Gln	Tyr	Lys	Lys	Leu	Arg	Glu	Ala	Ile	Asp	Lys	165	170	175	
Tyr	Glu	Gly	Gly	Leu	Glu	Ala	Phe	Ser	Arg	Gly	Tyr	Glu	Lys	Met	Gly	180	185	190	
Phe	Thr	Arg	Ser	Ala	Thr	Gly	Ile	Thr	Tyr	Arg	Glu	Trp	Ala	Pro	Gly	195	200	205	
Ala	Gln	Ser	Ala	Ala	Leu	Ile	Gly	Asp	Phe	Asn	Asn	Trp	Asp	Ala	Asn	210	215	220	
Ala	Asp	Ile	Met	Thr	Arg	Asn	Glu	Phe	Gly	Val	Trp	Glu	Ile	Phe	Leu	225	230	235	240
Pro	Asn	Asn	Val	Asp	Gly	Ser	Pro	Ala	Ile	Pro	His	Gly	Ser	Arg	Val	245	250	255	
Lys	Ile	Arg	Met	Asp	Thr	Pro	Ser	Gly	Val	Lys	Asp	Ser	Ile	Pro	Ala	260	265	270	
Trp	Ile	Asn	Tyr	Ser	Ser	Gln	Leu	Pro	Asp	Glu	Ile	Pro	Tyr	Asn	Gly	275	280	285	
Ile	Tyr	Tyr	Asp	Pro	Pro	Glu	Glu	Glu	Arg	Tyr	Ile	Phe	Gln	His	Pro	290	295	300	
Arg	Pro	Lys	Lys	Pro	Lys	Ser	Leu	Arg	Ile	Tyr	Glu	Ser	His	Ile	Gly	305	310	315	320
Met	Ser	Ser	Pro	Glu	Pro	Lys	Ile	Asn	Ser	Tyr	Val	Asn	Phe	Arg	Asp	325	330	335	
Glu	Val	Leu	Pro	Arg	Ile	Lys	Lys	Leu	Gly	Tyr	Asn	Ala	Val	Gln	Ile	340	345	350	

Met	Ala	Ile	Gln	Glu	His	Ser	Tyr	Tyr	Ala	Ser	Phe	Gly	Tyr	His	Val	355	360	365	
Thr	Asn	Phe	Phe	Ala	Pro	Ser	Ser	Arg	Phe	Gly	Thr	Pro	Asp	Asp	Leu	370	375	380	
Lys	Ser	Leu	Ile	Asp	Lys	Ala	His	Glu	Leu	Gly	Ile	Val	Val	Leu	Met	385	390	395	400
Asp	Ile	Val	His	Ser	His	Ala	Ser	Asn	Asn	Thr	Leu	Asp	Gly	Leu	Asn	405	410	415	
Met	Phe	Asp	Gly	Thr	Asp	Ser	Cys	Tyr	Phe	His	Ser	Gly	Ala	Arg	Gly	420	425	430	
Tyr	His	Trp	Met	Trp	Asp	Ser	Arg	Leu	Phe	Asn	Tyr	Gly	Asn	Trp	Glu	435	440	445	
Val	Leu	Arg	Tyr	Leu	Leu	Ser	Asn	Ala	Arg	Trp	Trp	Leu	Asp	Glu	Phe	450	455	460	
Lys	Phe	Asp	Gly	Phe	Arg	Phe	Asp	Gly	Val	Thr	Ser	Met	Met	Tyr	Thr	465	470	475	480
His	His	Gly	Leu	Ser	Val	Gly	Phe	Thr	Gly	Asn	Tyr	Glu	Glu	Tyr	Phe	485	490	495	
Gly	Leu	Ala	Thr	Asp	Val	Asp	Ala	Val	Val	Tyr	Leu	Met	Leu	Val	Asn	500	505	510	
Asp	Leu	Ile	His	Gly	Leu	Phe	Pro	Asp	Ala	Ile	Thr	Ile	Gly	Glu	Asp	515	520	525	
Val	Ser	Gly	Met	Pro	Thr	Phe	Cys	Ile	Pro	Val	Gln	Asp	Gly	Gly	Val	530	535	540	
Gly	Phe	Asp	Tyr	Arg	Leu	His	Met	Ala	Ile	Ala	Asp	Lys	Trp	Ile	Glu	545	550	555	560
Leu	Leu	Lys	Lys	Arg	Asp	Glu	Asp	Trp	Arg	Val	Gly	Asp	Ile	Val	His	565	570	575	
Thr	Leu	Thr	Asn	Arg	Arg	Trp	Ser	Glu	Lys	Cys	Val	Ser	Tyr	Ala	Glu	580	585	590	
Ser	His	Asp	Gln	Ala	Leu	Val	Gly	Asp	Lys	Thr	Ile	Ala	Phe	Trp	Leu	595	600	605	
Met	Asp	Lys	Asp	Met	Tyr	Asp	Phe	Met	Ala	Leu	Asp	Arg	Pro	Pro	Thr	610	615	620	
Ser	Leu	Ile	Asp	Arg	Gly	Ile	Ala	Leu	His	Lys	Met	Ile	Arg	Leu	Val	625	630	635	640

Thr Met Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu  
                                 645                                650                                655  
 Phe Gly His Pro Glu Trp Ile Asp Phe Pro Arg Ala Glu Gln His Leu  
                                 660                                665                                670  
 Ser Asp Asp Ser Val Ile Pro Gly Asn Gln Phe Ser Tyr Asp Lys Cys  
                                 675                                680                                685  
 Arg Arg Arg Phe Asp Leu Gly Asp Ala Glu Tyr Leu Arg Tyr Arg Gly  
                                 690                                695                                700  
 Leu Gln Glu Phe Asp Arg Ala Met Gln Tyr Leu Glu Asp Lys Tyr Glu  
                                 705                                710                                715                                720  
 Phe Met Thr Ser Glu His Gln Phe Ile Ser Arg Lys Asp Glu Gly Asp  
                                 725                                730                                735  
 Arg Met Ile Val Phe Glu Lys Gly Asn Leu Val Phe Val Phe Asn Phe  
                                 740                                745                                750  
 His Trp Thr Lys Ser Tyr Ser Asp Tyr Arg Ile Gly Cys Leu Lys Pro  
                                 755                                760                                765  
 Gly Lys Tyr Lys Val Ala Leu Asp Ser Asp Asp Pro Leu Phe Gly Gly  
                                 770                                775                                780  
 Phe Gly Arg Ile Asp His Asn Ala Glu Tyr Phe Thr Phe Glu Gly Trp  
                                 785                                790                                795                                800  
 Tyr Asp Asp Arg Pro Arg Ser Ile Met Val Tyr Ala Pro Cys Arg Thr  
                                 805                                810                                815  
 Ala Val Val Tyr Ala Leu Val Asp Lys Glu Glu Glu Glu Glu Glu Glu  
                                 820                                825                                830  
 Glu Glu Glu Val Ala Val Val Glu Glu Val Val Val Glu Glu Glu  
                                 835                                840                                845

<210> 43

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 43

Met Asn Lys Arg Ile Asp Leu

1

5